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| <p>(71) Applicant: CORIXA CORPORATION [US/US]; Suite 200, 1124 Columbia Street, Seattle, WA 98104 (US).</p> <p>(72) Inventors: XU, Jiangchun; 15805 Southeast 43rd Place, Bellevue, WA 98006 (US). DILLON, Davin, C.; 21607 N.E. 24th Street, Redmond, WA 98053 (US).</p> <p>(74) Agents: MAKI, David, J. et al.; Seed and Berry LLP, 6300 Columbia Center, 701 Fifth Avenue, Seattle, WA 98104-7092 (US).</p> | | | | | | | | | | | | |
| <p>(54) Title: COMPOUNDS FOR IMMUNOTHERAPY OF PROSTATE CANCER AND METHODS FOR THEIR USE</p> <p>(57) Abstract</p> <p>Compounds and methods for treating prostate cancer are provided. The inventive compounds include polypeptides containing at least a portion of a prostate tumor protein. Vaccines and pharmaceutical compositions for immunotherapy of prostate cancer comprising such polypeptides, or DNA molecules encoding such polypeptides, are also provided, together with DNA molecules for preparing the inventive polypeptides.</p> | | | | | | | | | | | | |

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COMPOUNDS FOR IMMUNOTHERAPY
OF PROSTATE CANCER AND METHODS FOR THEIR USE

TECHNICAL FIELD

The present invention relates generally to compositions and methods for the treatment of prostate cancer. The invention is more particularly related to polypeptides comprising at least a portion of a prostate protein and to DNA molecules encoding such polypeptides. Such polypeptides may be used in vaccines and pharmaceutical compositions for treatment of prostate cancer.

BACKGROUND OF THE INVENTION

Prostate cancer is the most common form of cancer among males, with an estimated incidence of 30% in men over the age of 50. Overwhelming clinical evidence shows that human prostate cancer has the propensity to metastasize to bone, and the disease appears to progress inevitably from androgen dependent to androgen refractory status, leading to increased patient mortality. This prevalent disease is currently the second leading cause of cancer death among men in the U.S.

In spite of considerable research into therapies for the disease, prostate cancer remains difficult to treat. Commonly, treatment is based on surgery and/or radiation therapy, but these methods are ineffective in a significant percentage of cases. Two previously identified prostate specific proteins - prostate specific antigen (PSA) and prostatic acid phosphatase (PAP) - have limited therapeutic and diagnostic potential. For example, PSA levels do not always correlate well with the presence of prostate cancer, being positive in a percentage of non-prostate cancer cases, including benign prostatic hyperplasia (BPH). Furthermore, PSA measurements correlate with prostate volume, and do not indicate the level of metastasis.

Accordingly, there remains a need in the art for improved vaccines and treatment methods for prostate cancer.

SUMMARY OF THE INVENTION

The present invention provides compounds and methods for immunotherapy of prostate cancer. In one aspect, polypeptides are provided comprising at least an immunogenic portion of a prostate tumor protein or a variant of said protein that differs only in conservative substitutions and/or modifications, wherein the prostate tumor protein comprises an amino acid sequence encoded by a DNA molecule having a sequence selected from the group consisting of nucleotide sequences recited in SEQ ID NO: 2, 3, 8-29, 41-45, 47-52, 54-65, 70, 73-74, 79, 81, 87, 90, 92, 93, 97, 103, 104, 107, 109-111, 115-160, 171, 173-175, 177, 181, 188, 191, 193, 194, 198, 203, 204, 207, 209-211, 220, 222-224, the complements of said nucleotide sequences and variants thereof.

In related aspects, DNA molecules encoding the above polypeptides are provided. In specific embodiments, such DNA molecules include sequences provided in SEQ ID NO: 2, 3, 8-29, 41-45, 47-52, 54-65, 70, 73-74, 79, 81, 87, 90, 92, 93, 97, 103, 104, 107, 109-111, 115-160, 171, 173-175, 177, 181, 188, 191, 193, 194, 198, 203, 204, 207, 209-211, 220 and 222-224. The present invention further provides expression vectors comprising the above DNA molecules and host cells transformed or transfected with such expression vectors. In preferred embodiments, the host cells are selected from the group consisting of *E. coli*, yeast and mammalian cells.

In another aspect, the present invention provides fusion proteins comprising a first and a second inventive polypeptide or, alternatively, an inventive polypeptide and a known prostate antigen.

The present invention also provides pharmaceutical compositions comprising one or more of the above polypeptides, or a DNA molecule encoding such polypeptides, and a physiologically acceptable carrier, together with vaccines comprising one or more of such polypeptide or DNA molecules in combination with a non-specific immune response enhancer.

In related aspects, pharmaceutical compositions for the treatment of prostate cancer comprising one or more polypeptides and a physiologically acceptable carrier are provided, wherein the polypeptide comprises an immunogenic portion of a prostate tumor protein or of a variant of said protein that differs only in conservative substitutions and/or modifications, the prostate tumor protein being encoded by a DNA molecule having a

sequence selected from the group consisting of nucleotide sequences recited in SEQ ID NO: 5-7, 30-40, 46, 53, 66-69, 71, 72, 75-78, 80, 82-86, 88, 89, 91, 94-96, 98-102, 105, 106 and 161-170, 179, 180, 182-187, 189, 190, 192, 195-197, 199-202, 205, 206, 208, 212-219, 221, the complements of said nucleotide sequences and variants thereof. The invention also provides vaccines for the treatment of prostate cancer comprising such polypeptides in combination with a non-specific immune response enhancer, together with pharmaceutical compositions and vaccines comprising one or more DNA molecules having a sequence provided in SEQ ID NO: 5-7, 30-40, 46, 53, 66-69, 71, 72, 75-78, 80, 82-86, 88, 89, 91, 94-96, 98-102, 105, 106 and 161-170, 179, 180, 182-187, 189, 190, 192, 195-197, 199-202, 205, 206, 208, 212-219 and 221. Pharmaceutical compositions and vaccines comprising one or more of the above fusion proteins are also provided.

In yet another aspect, methods are provided for inhibiting the development of prostate cancer in a patient, comprising administering an effective amount of at least one of the above pharmaceutical compositions and/or vaccines.

These and other aspects of the present invention will become apparent upon reference to the following detailed description and attached drawings. All references disclosed herein are hereby incorporated by reference in their entirety as if each was incorporated individually.

DETAILED DESCRIPTION OF THE INVENTION

As noted above, the present invention is generally directed to compositions and methods for the immunotherapy of prostate cancer. The inventive compositions are generally polypeptides that comprise at least a portion of a prostate tumor protein. Also included within the present invention are molecules (such as an antibody or fragment thereof) that bind to the inventive polypeptides. Such molecules are referred to herein as "binding agents."

In particular, the subject invention discloses polypeptides comprising at least a portion of a human prostate tumor protein, or a variant of such a protein that differs only in conservative substitutions and/or modifications, wherein the prostate tumor protein includes an amino acid sequence encoded by a DNA molecule having a sequence selected from the group consisting of nucleotide sequences recited in SEQ ID NO: 2, 3, 8-29, 41-45, 47-52, 54-

65, 70, 73-74, 79, 81, 87, 90, 92, 93, 97, 103, 104, 107, 109-111, 115-160, 181, 188, 191, 193, 194, 198, 203, 204, and 207-224, the complements of said nucleotide sequences and variants thereof. As used herein, the term "polypeptide" encompasses amino acid chains of any length, including full length proteins, wherein the amino acid residues are linked by covalent peptide bonds. Thus, a polypeptide comprising a portion of one of the above prostate proteins may consist entirely of the portion, or the portion may be present within a larger polypeptide that contains additional sequences. The additional sequences may be derived from the native protein or may be heterologous, and such sequences may be immunoreactive and/or antigenic.

As used herein, an "immunogenic portion" of a human prostate tumor protein is a portion that is capable of eliciting an immune response in a patient inflicted with prostate cancer and as such binds to antibodies present within sera from a prostate cancer patient. Immunogenic portions of the proteins described herein may thus be identified in antibody binding assays. Such assays may generally be performed using any of a variety of means known to those of ordinary skill in the art, as described, for example, in Harlow and Lane, *Antibodies: A Laboratory Manual*, Cold Spring Harbor Laboratory, Cold Spring Harbor, NY, 1988. For example, a polypeptide may be immobilized on a solid support (as described below) and contacted with patient sera to allow binding of antibodies within the sera to the immobilized polypeptide. Unbound sera may then be removed and bound antibodies detected using, for example, ¹²⁵I-labeled Protein A. Alternatively, a polypeptide may be used to generate monoclonal and polyclonal antibodies for use in detection of the polypeptide in blood or other fluids of prostate cancer patients.

The compositions and methods of the present invention also encompass variants of the above polypeptides and DNA molecules. A polypeptide "variant," as used herein, is a polypeptide that differs from the recited polypeptide only in conservative substitutions and/or modifications, such that the therapeutic, antigenic and/or immunogenic properties of the polypeptide are retained. Polypeptide variants preferably exhibit at least about 70%, more preferably at least about 90% and most preferably at least about 95% identity to the identified polypeptides. For prostate tumor polypeptides with immunoreactive properties, variants may, alternatively, be identified by modifying the amino acid sequence of

one of the above polypeptides, and evaluating the immunoreactivity of the modified polypeptide. For prostate tumor polypeptides useful for the generation of diagnostic binding agents, a variant may be identified by evaluating a modified polypeptide for the ability to generate antibodies that detect the presence or absence of prostate cancer. Such modified sequences may be prepared and tested using, for example, the representative procedures described herein.

As used herein, a "conservative substitution" is one in which an amino acid is substituted for another amino acid that has similar properties, such that one skilled in the art of peptide chemistry would expect the secondary structure and hydropathic nature of the polypeptide to be substantially unchanged. In general, the following groups of amino acids represent conservative changes: (1) ala, pro, gly, glu, asp, gln, asn, ser, thr; (2) cys, ser, tyr, thr; (3) val, ile, leu, met, ala, phe; (4) lys, arg, his; and (5) phe, tyr, trp, his.

Variants may also, or alternatively, contain other modifications, including the deletion or addition of amino acids that have minimal influence on the antigenic properties, secondary structure and hydropathic nature of the polypeptide. For example, a polypeptide may be conjugated to a signal (or leader) sequence at the N-terminal end of the protein which co-translationally or post-translationally directs transfer of the protein. The polypeptide may also be conjugated to a linker or other sequence for ease of synthesis, purification or identification of the polypeptide (e.g., poly-His), or to enhance binding of the polypeptide to a solid support. For example, a polypeptide may be conjugated to an immunoglobulin Fc region.

A nucleotide "variant" is a sequence that differs from the recited nucleotide sequence in having one or more nucleotide deletions, substitutions or additions. Such modifications may be readily introduced using standard mutagenesis techniques, such as oligonucleotide-directed site-specific mutagenesis as taught, for example, by Adelman et al. (*DNA*, 2:183, 1983). Nucleotide variants may be naturally occurring allelic variants, or non-naturally occurring variants. Variant nucleotide sequences preferably exhibit at least about 70%, more preferably at least about 80% and most preferably at least about 90% identity to the recited sequence. Such variant nucleotide sequences will generally hybridize to the recited nucleotide sequence under stringent conditions. As used herein, "stringent conditions" refers

to prewashing in a solution of 6X SSC, 0.2% SDS; hybridizing at 65 °C, 6X SSC, 0.2% SDS overnight; followed by two washes of 30 minutes each in 1X SSC, 0.1% SDS at 65 °C and two washes of 30 minutes each in 0.2X SSC, 0.1% SDS at 65 °C.

"Polypeptides" as used herein also include combination, or fusion, polypeptides. A "combination polypeptide" is a polypeptide comprising at least one of the above immunogenic portions and one or more additional immunogenic prostate tumor-specific sequences, which are joined via a peptide linkage into a single amino acid chain. The sequences may be joined directly (*i.e.*, with no intervening amino acids) or may be joined by way of a linked sequence (*e.g.*, Gly-Cys-Gly) that does not significantly diminish the immunogenic properties of the component polypeptides.

The prostate tumor proteins of the present invention, and DNA molecules encoding such proteins, may be isolated from prostatic tumor tissue using any of a variety of methods well known in the art. DNA sequences corresponding to a gene (of a portion thereof) encoding one of the inventive prostate tumor proteins may be isolated from a prostate tumor cDNA library using a subtraction technique as described in detail below. Examples of such DNA sequences are provided in SEQ ID NOS: 1-107, 109-111, 115-171, 173-175, 177 and 179-224. Partial DNA sequences thus obtained may be used to design oligonucleotide primers for the amplification of full-length DNA sequences in a polymerase chain reaction (PCR), using techniques well known in the art (see, for example, Mullis et al., *Cold Spring Harbor Symp. Quant. Biol.*, 51:263, 1987; Erlich ed., *PCR Technology*, Stockton Press, NY, 1989). Once a DNA sequence encoding a polypeptide is obtained, any of the above modifications may be readily introduced using standard mutagenesis techniques, such as oligonucleotide-directed site-specific mutagenesis as taught, for example, by Adelman et al. (*DNA*, 2:183, 1983).

The prostate tumor polypeptides disclosed herein may also be generated by synthetic or recombinant means. Synthetic polypeptides having fewer than about 100 amino acids, and generally fewer than about 50 amino acids, may be generated using techniques well known to those of ordinary skill in the art. For example, such polypeptides may be synthesized using any of the commercially available solid-phase techniques, such as the Merrifield solid-phase synthesis method, where amino acids are sequentially added to a

growing amino acid chain (see, for example, Merrifield, *J. Am. Chem. Soc.* 85:2149-2146, 1963). Equipment for automated synthesis of polypeptides is commercially available from suppliers such as Perkin Elmer/Applied BioSystems Division (Foster City, CA), and may be operated according to the manufacturer's instructions.

Alternatively, any of the above polypeptides may be produced recombinantly by inserting a DNA sequence that encodes the polypeptide into an expression vector and expressing the protein in an appropriate host. Any of a variety of expression vectors known to those of ordinary skill in the art may be employed to express recombinant polypeptides of this invention. Expression may be achieved in any appropriate host cell that has been transformed or transfected with an expression vector containing a DNA molecule that encodes a recombinant polypeptide. Suitable host cells include prokaryotes, yeast and higher eukaryotic cells. Preferably, the host cells employed are *E. coli*, yeast or a mammalian cell line, such as CHO cells. The DNA sequences expressed in this manner may encode naturally occurring polypeptides, portions of naturally occurring polypeptides, or other variants thereof.

In general, regardless of the method of preparation, the polypeptides disclosed herein are prepared in substantially pure form (*i.e.*, the polypeptides are homogenous as determined by amino acid composition and primary sequence analysis). Preferably, the polypeptides are at least about 90% pure, more preferably at least about 95% pure and most preferably at least about 99% pure. In certain preferred embodiments, described in more detail below, the substantially pure polypeptides are incorporated into pharmaceutical compositions or vaccines for use in one or more of the methods disclosed herein.

In a related aspect, the present invention provides fusion proteins comprising a first and a second inventive polypeptide or, alternatively, a polypeptide of the present invention and a known prostate antigen, together with variants of such fusion proteins. The fusion proteins of the present invention may also include a linker peptide between the first and second polypeptides.

A DNA sequence encoding a fusion protein of the present invention is constructed using known recombinant DNA techniques to assemble separate DNA sequences encoding the first and second polypeptides into an appropriate expression vector. The 3' end

of a DNA sequence encoding the first polypeptide is ligated, with or without a peptide linker, to the 5' end of a DNA sequence encoding the second polypeptide so that the reading frames of the sequences are in phase to permit mRNA translation of the two DNA sequences into a single fusion protein that retains the biological activity of both the first and the second polypeptides.

A peptide linker sequence may be employed to separate the first and the second polypeptides by a distance sufficient to ensure that each polypeptide folds into its secondary and tertiary structures. Such a peptide linker sequence is incorporated into the fusion protein using standard techniques well known in the art. Suitable peptide linker sequences may be chosen based on the following factors: (1) their ability to adopt a flexible extended conformation; (2) their inability to adopt a secondary structure that could interact with functional epitopes on the first and second polypeptides; and (3) the lack of hydrophobic or charged residues that might react with the polypeptide functional epitopes. Preferred peptide linker sequences contain Gly, Asn and Ser residues. Other near neutral amino acids, such as Thr and Ala may also be used in the linker sequence. Amino acid sequences which may be usefully employed as linkers include those disclosed in Maratea et al., *Gene* 40:39-46, 1985; Murphy et al., *Proc. Natl. Acad. Sci. USA* 83:8258-8262, 1986; U.S. Patent No. 4,935,233 and U.S. Patent No. 4,751,180. The linker sequence may be from 1 to about 50 amino acids in length. Peptide sequences are not required when the first and second polypeptides have non-essential N-terminal amino acid regions that can be used to separate the functional domains and prevent steric interference.

The ligated DNA sequences are operably linked to suitable transcriptional or translational regulatory elements. The regulatory elements responsible for expression of DNA are located only 5' to the DNA sequence encoding the first polypeptides. Similarly, stop codons require to end translation and transcription termination signals are only present 3' to the DNA sequence encoding the second polypeptide.

Polypeptides of the present invention that comprise an immunogenic portion of a prostate tumor protein may generally be used for immunotherapy of prostate cancer, wherein the polypeptide stimulates the patient's own immune response to prostate tumor cells. In further aspects, the present invention provides methods for using one or more of the

immunoreactive polypeptides encoded by a DNA molecule having a sequence provided in SEQ ID NOS: 1-107, 109-111, 115-171, 173-175, 177 and 179-224 (or fusion proteins comprising one or more such polypeptides and/or DNA encoding such polypeptides) for immunotherapy of prostate cancer in a patient. As used herein, a "patient" refers to any warm-blooded animal, preferably a human. A patient may be afflicted with a disease, or may be free of detectable disease. Accordingly, the above immunoreactive polypeptides (or fusion proteins or DNA molecules encoding such polypeptides) may be used to treat prostate cancer or to inhibit the development of prostate cancer. The polypeptides may be administered either prior to or following surgical removal of primary tumors and/or treatment by administration of radiotherapy and conventional chemotherapeutic drugs.

In these aspects, the polypeptide or fusion protein is generally present within a pharmaceutical composition and/or a vaccine. Pharmaceutical compositions may comprise one or more polypeptides, each of which may contain one or more of the above sequences (or variants thereof), and a physiologically acceptable carrier. The vaccines may comprise one or more of such polypeptides and a non-specific immune response enhancer, such as an adjuvant, biodegradable microsphere (*e.g.*, polylactic galactide) or a liposome (into which the polypeptide is incorporated). Pharmaceutical compositions and vaccines may also contain other epitopes of prostate tumor antigens, either incorporated into a combination polypeptide (*i.e.*, a single polypeptide that contains multiple epitopes) or present within a separate polypeptide.

Alternatively, a pharmaceutical composition or vaccine may contain DNA encoding one or more of the above polypeptides, such that the polypeptide is generated *in situ*. In such pharmaceutical compositions and vaccines, the DNA may be present within any of a variety of delivery systems known to those of ordinary skill in the art, including nucleic acid expression systems, bacteria and viral expression systems. Appropriate nucleic acid expression systems contain the necessary DNA sequences for expression in the patient (such as a suitable promoter). Bacterial delivery systems involve the administration of a bacterium (such as *Bacillus-Calmette-Guerin*) that expresses an epitope of a prostate cell antigen on its cell surface. In a preferred embodiment, the DNA may be introduced using a viral expression system (*e.g.*, vaccinia or other pox virus, retrovirus, or adenovirus), which may involve the

use of a non-pathogenic (defective), replication competent virus. Suitable systems are disclosed, for example, in Fisher-Hoch et al., *PNAS* 86:317-321, 1989; Flexner et al., *Ann. N.Y. Acad. Sci.* 569:86-103, 1989; Flexner et al., *Vaccine* 8:17-21, 1990; U.S. Patent Nos. 4,603,112, 4,769,330, and 5,017,487; WO 89/01973; U.S. Patent No. 4,777,127; GB 2,200,651; EP 0,345,242; WO 91/02805; Berkner, *Biotechniques* 6:616-627, 1988; Rosenfeld et al., *Science* 252:431-434, 1991; Kolls et al., *PNAS* 91:215-219, 1994; Kass-Eisler et al., *PNAS* 90:11498-11502, 1993; Guzman et al., *Circulation* 88:2838-2848, 1993; and Guzman et al., *Cir. Res.* 73:1202-1207, 1993. Techniques for incorporating DNA into such expression systems are well known to those of ordinary skill in the art. The DNA may also be "naked," as described, for example, in published PCT application WO 90/11092, and Ulmer et al., *Science* 259:1745-1749, 1993, reviewed by Cohen, *Science* 259:1691-1692, 1993. The uptake of naked DNA may be increased by coating the DNA onto biodegradable beads, which are efficiently transported into the cells.

Routes and frequency of administration, as well as dosage, will vary from individual to individual and may parallel those currently being used in immunotherapy of other diseases. In general, the pharmaceutical compositions and vaccines may be administered by injection (e.g., intracutaneous, intramuscular, intravenous or subcutaneous), intranasally (e.g., by aspiration) or orally. Between 1 and 10 doses may be administered over a 3-24 week period. Preferably, 4 doses are administered, at an interval of 3 months, and booster administrations may be given periodically thereafter. Alternate protocols may be appropriate for individual patients. A suitable dose is an amount of polypeptide or DNA that is effective to raise an immune response (cellular and/or humoral) against prostate tumor cells in a treated patient. A suitable immune response is at least 10-50% above the basal (i.e., untreated) level. In general, the amount of polypeptide present in a dose (or produced *in situ* by the DNA in a dose) ranges from about 1 pg to about 100 mg per kg of host, typically from about 10 pg to about 1 mg, and preferably from about 100 pg to about 1 µg. Suitable dose sizes will vary with the size of the patient, but will typically range from about 0.01 mL to about 5 mL.

While any suitable carrier known to those of ordinary skill in the art may be employed in the pharmaceutical compositions of this invention, the type of carrier will vary

depending on the mode of administration. For parenteral administration, such as subcutaneous injection, the carrier preferably comprises water, saline, alcohol, a lipid, a wax and/or a buffer. For oral administration, any of the above carriers or a solid carrier, such as mannitol, lactose, starch, magnesium stearate, sodium saccharine, talcum, cellulose, glucose, sucrose, and/or magnesium carbonate, may be employed. Biodegradable microspheres (e.g., polylactic glycolide) may also be employed as carriers for the pharmaceutical compositions of this invention. Suitable biodegradable microspheres are disclosed, for example, in U.S. Patent Nos. 4,897,268 and 5,075,109.

Any of a variety of non-specific immune response enhancers may be employed in the vaccines of this invention. For example, an adjuvant may be included. Most adjuvants contain a substance designed to protect the antigen from rapid catabolism, such as aluminum hydroxide or mineral oil, and a nonspecific stimulator of immune response, such as lipid A, *Bordetella pertussis* or *Mycobacterium tuberculosis*. Such adjuvants are commercially available as, for example, Freund's Incomplete Adjuvant and Complete Adjuvant (Difco Laboratories, Detroit, MI) and Merck Adjuvant 65 (Merck and Company, Inc., Rahway, NJ).

Polypeptides disclosed herein may also be employed in *ex vivo* treatment of prostate cancer. For example, cells of the immune system, such as T cells, may be isolated from the peripheral blood of a patient, using a commercially available cell separation system, such as CellPro Incorporated's (Bothell, WA) CEPRATE™ system (see U.S. Patent No. 5,240,856; U.S. Patent No. 5,215,926; WO 89/06280; WO 91/16116 and WO 92/07243). The separated cells are stimulated with one or more of the immunoreactive polypeptides contained within a delivery vehicle, such as a microsphere, to provide antigen-specific T cells. The population of tumor antigen-specific T cells is then expanded using standard techniques and the cells are administered back to the patient.

Polypeptides of the present invention may also, or alternatively, be used to generate binding agents, such as antibodies or fragments thereof, that are capable of detecting metastatic human prostate tumors. Binding agents of the present invention may generally be prepared using methods known to those of ordinary skill in the art, including the representative procedures described herein. Binding agents are capable of differentiating between patients with and without prostate cancer, using the representative assays described

herein. In other words, antibodies or other binding agents raised against a prostate tumor protein, or a suitable portion thereof, will generate a signal indicating the presence of primary or metastatic prostate cancer in at least about 20% of patients afflicted with the disease, and will generate a negative signal indicating the absence of the disease in at least about 90% of individuals without primary or metastatic prostate cancer. Suitable portions of such prostate tumor proteins are portions that are able to generate a binding agent that indicates the presence of primary or metastatic prostate cancer in substantially all (*i.e.*, at least about 80%, and preferably at least about 90%) of the patients for which prostate cancer would be indicated using the full length protein, and that indicate the absence of prostate cancer in substantially all of those samples that would be negative when tested with full length protein. The representative assays described below, such as the two-antibody sandwich assay, may generally be employed for evaluating the ability of a binding agent to detect metastatic human prostate tumors.

The ability of a polypeptide prepared as described herein to generate antibodies capable of detecting primary or metastatic human prostate tumors may generally be evaluated by raising one or more antibodies against the polypeptide (using, for example, a representative method described herein) and determining the ability of such antibodies to detect such tumors in patients. This determination may be made by assaying biological samples from patients with and without primary or metastatic prostate cancer for the presence of a polypeptide that binds to the generated antibodies. Such test assays may be performed, for example, using a representative procedure described below. Polypeptides that generate antibodies capable of detecting at least 20% of primary or metastatic prostate tumors by such procedures are considered to be useful in assays for detecting primary or metastatic human prostate tumors. Polypeptide specific antibodies may be used alone or in combination to improve sensitivity.

Polypeptides capable of detecting primary or metastatic human prostate tumors may be used as markers for diagnosing prostate cancer or for monitoring disease progression in patients. In one embodiment, prostate cancer in a patient may be diagnosed by evaluating a biological sample obtained from the patient for the level of one or more of the

above polypeptides, relative to a predetermined cut-off value. As used herein, suitable "biological samples" include blood, sera, urine and/or prostate secretions.

The level of one or more of the above polypeptides may be evaluated using any binding agent specific for the polypeptide(s). A "binding agent," in the context of this invention, is any agent (such as a compound or a cell) that binds to a polypeptide as described above. As used herein, "binding" refers to a noncovalent association between two separate molecules (each of which may be free (*i.e.*, in solution) or present on the surface of a cell or a solid support), such that a "complex" is formed. Such a complex may be free or immobilized (either covalently or noncovalently) on a support material. The ability to bind may generally be evaluated by determining a binding constant for the formation of the complex. The binding constant is the value obtained when the concentration of the complex is divided by the product of the component concentrations. In general, two compounds are said to "bind" in the context of the present invention when the binding constant for complex formation exceeds about 10^3 L/mol. The binding constant may be determined using methods well known to those of ordinary skill in the art.

Any agent that satisfies the above requirements may be a binding agent. For example, a binding agent may be a ribosome with or without a peptide component, an RNA molecule or a peptide. In a preferred embodiment, the binding partner is an antibody, or a fragment thereof. Such antibodies may be polyclonal, or monoclonal. In addition, the antibodies may be single chain, chimeric, CDR-grafted or humanized. Antibodies may be prepared by the methods described herein and by other methods well known to those of skill in the art.

There are a variety of assay formats known to those of ordinary skill in the art for using a binding partner to detect polypeptide markers in a sample. *See, e.g.*, Harlow and Lane, *Antibodies: A Laboratory Manual*, Cold Spring Harbor Laboratory, 1988. In a preferred embodiment, the assay involves the use of binding partner immobilized on a solid support to bind to and remove the polypeptide from the remainder of the sample. The bound polypeptide may then be detected using a second binding partner that contains a reporter group. Suitable second binding partners include antibodies that bind to the binding partner/polypeptide complex. Alternatively, a competitive assay may be utilized, in which a

polypeptide is labeled with a reporter group and allowed to bind to the immobilized binding partner after incubation of the binding partner with the sample. The extent to which components of the sample inhibit the binding of the labeled polypeptide to the binding partner is indicative of the reactivity of the sample with the immobilized binding partner.

The solid support may be any material known to those of ordinary skill in the art to which the antigen may be attached. For example, the solid support may be a test well in a microtiter plate or a nitrocellulose or other suitable membrane. Alternatively, the support may be a bead or disc, such as glass, fiberglass, latex or a plastic material such as polystyrene or polyvinylchloride. The support may also be a magnetic particle or a fiber optic sensor, such as those disclosed, for example, in U.S. Patent No. 5,359,681. The binding agent may be immobilized on the solid support using a variety of techniques known to those of skill in the art, which are amply described in the patent and scientific literature. In the context of the present invention, the term "immobilization" refers to both noncovalent association, such as adsorption, and covalent attachment (which may be a direct linkage between the antigen and functional groups on the support or may be a linkage by way of a cross-linking agent). Immobilization by adsorption to a well in a microtiter plate or to a membrane is preferred. In such cases, adsorption may be achieved by contacting the binding agent, in a suitable buffer, with the solid support for a suitable amount of time. The contact time varies with temperature, but is typically between about 1 hour and about 1 day. In general, contacting a well of a plastic microtiter plate (such as polystyrene or polyvinylchloride) with an amount of binding agent ranging from about 10 ng to about 10 µg, and preferably about 100 ng to about 1 µg, is sufficient to immobilize an adequate amount of binding agent.

Covalent attachment of binding agent to a solid support may generally be achieved by first reacting the support with a bifunctional reagent that will react with both the support and a functional group, such as a hydroxyl or amino group, on the binding agent. For example, the binding agent may be covalently attached to supports having an appropriate polymer coating using benzoquinone or by condensation of an aldehyde group on the support with an amine and an active hydrogen on the binding partner (see, e.g., Pierce Immunotechnology Catalog and Handbook, 1991, at A12-A13).

In certain embodiments, the assay is a two-antibody sandwich assay. This assay may be performed by first contacting an antibody that has been immobilized on a solid support, commonly the well of a microtiter plate, with the sample, such that polypeptides within the sample are allowed to bind to the immobilized antibody. Unbound sample is then removed from the immobilized polypeptide-antibody complexes and a second antibody (containing a reporter group) capable of binding to a different site on the polypeptide is added. The amount of second antibody that remains bound to the solid support is then determined using a method appropriate for the specific reporter group.

More specifically, once the antibody is immobilized on the support as described above, the remaining protein binding sites on the support are typically blocked. Any suitable blocking agent known to those of ordinary skill in the art, such as bovine serum albumin or Tween 20TM (Sigma Chemical Co., St. Louis, MO). The immobilized antibody is then incubated with the sample, and polypeptide is allowed to bind to the antibody. The sample may be diluted with a suitable diluent, such as phosphate-buffered saline (PBS) prior to incubation. In general, an appropriate contact time (*i.e.*, incubation time) is that period of time that is sufficient to detect the presence of polypeptide within a sample obtained from an individual with prostate cancer. Preferably, the contact time is sufficient to achieve a level of binding that is at least about 95% of that achieved at equilibrium between bound and unbound polypeptide. Those of ordinary skill in the art will recognize that the time necessary to achieve equilibrium may be readily determined by assaying the level of binding that occurs over a period of time. At room temperature, an incubation time of about 30 minutes is generally sufficient.

Unbound sample may then be removed by washing the solid support with an appropriate buffer, such as PBS containing 0.1% Tween 20TM. The second antibody, which contains a reporter group, may then be added to the solid support. Preferred reporter groups include enzymes (such as horseradish peroxidase), substrates, cofactors, inhibitors, dyes, radionuclides, luminescent groups, fluorescent groups and biotin. The conjugation of antibody to reporter group may be achieved using standard methods known to those of ordinary skill in the art.

The second antibody is then incubated with the immobilized antibody-polypeptide complex for an amount of time sufficient to detect the bound polypeptide. An appropriate amount of time may generally be determined by assaying the level of binding that occurs over a period of time. Unbound second antibody is then removed and bound second antibody is detected using the reporter group. The method employed for detecting the reporter group depends upon the nature of the reporter group. For radioactive groups, scintillation counting or autoradiographic methods are generally appropriate. Spectroscopic methods may be used to detect dyes, luminescent groups and fluorescent groups. Biotin may be detected using avidin, coupled to a different reporter group (commonly a radioactive or fluorescent group or an enzyme). Enzyme reporter groups may generally be detected by the addition of substrate (generally for a specific period of time), followed by spectroscopic or other analysis of the reaction products.

To determine the presence or absence of prostate cancer, the signal detected from the reporter group that remains bound to the solid support is generally compared to a signal that corresponds to a predetermined cut-off value. In one preferred embodiment, the cut-off value is the average mean signal obtained when the immobilized antibody is incubated with samples from patients without prostate cancer. In general, a sample generating a signal that is three standard deviations above the predetermined cut-off value is considered positive for prostate cancer. In an alternate preferred embodiment, the cut-off value is determined using a Receiver Operator Curve, according to the method of Sackett et al., *Clinical Epidemiology: A Basic Science for Clinical Medicine*, Little Brown and Co., 1985, p. 106-7. Briefly, in this embodiment, the cut-off value may be determined from a plot of pairs of true positive rates (*i.e.*, sensitivity) and false positive rates (100%-specificity) that correspond to each possible cut-off value for the diagnostic test result. The cut-off value on the plot that is the closest to the upper left-hand corner (*i.e.*, the value that encloses the largest area) is the most accurate cut-off value, and a sample generating a signal that is higher than the cut-off value determined by this method may be considered positive. Alternatively, the cut-off value may be shifted to the left along the plot, to minimize the false positive rate, or to the right, to minimize the false negative rate. In general, a sample generating a signal that is higher than the cut-off value determined by this method is considered positive for prostate cancer.

In a related embodiment, the assay is performed in a flow-through or strip test format, wherein the antibody is immobilized on a membrane, such as nitrocellulose. In the flow-through test, polypeptides within the sample bind to the immobilized antibody as the sample passes through the membrane. A second, labeled antibody then binds to the antibody-polypeptide complex as a solution containing the second antibody flows through the membrane. The detection of bound second antibody may then be performed as described above. In the strip test format, one end of the membrane to which antibody is bound is immersed in a solution containing the sample. The sample migrates along the membrane through a region containing second antibody and to the area of immobilized antibody. Concentration of second antibody at the area of immobilized antibody indicates the presence of prostate cancer. Typically, the concentration of second antibody at that site generates a pattern, such as a line, that can be read visually. The absence of such a pattern indicates a negative result. In general, the amount of antibody immobilized on the membrane is selected to generate a visually discernible pattern when the biological sample contains a level of polypeptide that would be sufficient to generate a positive signal in the two-antibody sandwich assay, in the format discussed above. Preferably, the amount of antibody immobilized on the membrane ranges from about 25 ng to about 1 μ g, and more preferably from about 50 ng to about 500 ng. Such tests can typically be performed with a very small amount of biological sample.

Of course, numerous other assay protocols exist that are suitable for use with the antigens or antibodies of the present invention. The above descriptions are intended to be exemplary only.

In another embodiment, the above polypeptides may be used as markers for the progression of prostate cancer. In this embodiment, assays as described above for the diagnosis of prostate cancer may be performed over time, and the change in the level of reactive polypeptide(s) evaluated. For example, the assays may be performed every 24-72 hours for a period of 6 months to 1 year, and thereafter performed as needed. In general, prostate cancer is progressing in those patients in whom the level of polypeptide detected by the binding agent increases over time. In contrast, prostate cancer is not progressing when the level of reactive polypeptide either remains constant or decreases with time.

Antibodies for use in the above methods may be prepared by any of a variety of techniques known to those of ordinary skill in the art. See, e.g., Harlow and Lane, *Antibodies: A Laboratory Manual*, Cold Spring Harbor Laboratory, 1988. In one such technique, an immunogen comprising the antigenic polypeptide is initially injected into any of a wide variety of mammals (e.g., mice, rats, rabbits, sheep and goats). In this step, the polypeptides of this invention may serve as the immunogen without modification. Alternatively, particularly for relatively short polypeptides, a superior immune response may be elicited if the polypeptide is joined to a carrier protein, such as bovine serum albumin or keyhole limpet hemocyanin. The immunogen is injected into the animal host, preferably according to a predetermined schedule incorporating one or more booster immunizations, and the animals are bled periodically. Polyclonal antibodies specific for the polypeptide may then be purified from such antisera by, for example, affinity chromatography using the polypeptide coupled to a suitable solid support.

Monoclonal antibodies specific for the antigenic polypeptide of interest may be prepared, for example, using the technique of Kohler and Milstein, *Eur. J. Immunol.* 6:511-519, 1976, and improvements thereto. Briefly, these methods involve the preparation of immortal cell lines capable of producing antibodies having the desired specificity (*i.e.*, reactivity with the polypeptide of interest). Such cell lines may be produced, for example, from spleen cells obtained from an animal immunized as described above. The spleen cells are then immortalized by, for example, fusion with a myeloma cell fusion partner, preferably one that is syngeneic with the immunized animal. A variety of fusion techniques may be employed. For example, the spleen cells and myeloma cells may be combined with a nonionic detergent for a few minutes and then plated at low density on a selective medium that supports the growth of hybrid cells, but not myeloma cells. A preferred selection technique uses HAT (hypoxanthine, aminopterin, thymidine) selection. After a sufficient time, usually about 1 to 2 weeks, colonies of hybrids are observed. Single colonies are selected and tested for binding activity against the polypeptide. Hybridomas having high reactivity and specificity are preferred.

Monoclonal antibodies may be isolated from the supernatants of growing hybridoma colonies. In addition, various techniques may be employed to enhance the yield,

such as injection of the hybridoma cell line into the peritoneal cavity of a suitable vertebrate host, such as a mouse. Monoclonal antibodies may then be harvested from the ascites fluid or the blood. Contaminants may be removed from the antibodies by conventional techniques, such as chromatography, gel filtration, precipitation, and extraction. The polypeptides of this invention may be used in the purification process in, for example, an affinity chromatography step.

Monoclonal antibodies of the present invention may also be used as therapeutic reagents, to diminish or eliminate prostate tumors. The antibodies may be used on their own (for instance, to inhibit metastases) or coupled to one or more therapeutic agents. Suitable agents in this regard include radionuclides, differentiation inducers, drugs, toxins, and derivatives thereof. Preferred radionuclides include ⁹⁰Y, ¹²³I, ¹²⁵I, ¹³¹I, ¹⁸⁶Re, ¹⁸⁸Re, ²¹¹At, and ²¹²Bi. Preferred drugs include methotrexate, and pyrimidine and purine analogs. Preferred differentiation inducers include phorbol esters and butyric acid. Preferred toxins include ricin, abrin, diphtheria toxin, cholera toxin, gelonin, Pseudomonas exotoxin, Shigella toxin, and pokeweed antiviral protein.

A therapeutic agent may be coupled (e.g., covalently bonded) to a suitable monoclonal antibody either directly or indirectly (e.g., via a linker group). A direct reaction between an agent and an antibody is possible when each possesses a substituent capable of reacting with the other. For example, a nucleophilic group, such as an amino or sulphydryl group, on one may be capable of reacting with a carbonyl-containing group, such as an anhydride or an acid halide, or with an alkyl group containing a good leaving group (e.g., a halide) on the other.

Alternatively, it may be desirable to couple a therapeutic agent and an antibody via a linker group. A linker group can function as a spacer to distance an antibody from an agent in order to avoid interference with binding capabilities. A linker group can also serve to increase the chemical reactivity of a substituent on an agent or an antibody, and thus increase the coupling efficiency. An increase in chemical reactivity may also facilitate the use of agents, or functional groups on agents, which otherwise would not be possible.

It will be evident to those skilled in the art that a variety of bifunctional or polyfunctional reagents, both homo- and hetero-functional (such as those described in the

catalog of the Pierce Chemical Co., Rockford, IL), may be employed as the linker group. Coupling may be effected, for example, through amino groups, carboxyl groups, sulphydryl groups or oxidized carbohydrate residues. There are numerous references describing such methodology, e.g., U.S. Patent No. 4,671,958, to Rodwell et al.

Where a therapeutic agent is more potent when free from the antibody portion of the immunoconjugates of the present invention, it may be desirable to use a linker group which is cleavable during or upon internalization into a cell. A number of different cleavable linker groups have been described. The mechanisms for the intracellular release of an agent from these linker groups include cleavage by reduction of a disulfide bond (e.g., U.S. Patent No. 4,489,710, to Spitzer), by irradiation of a photolabile bond (e.g., U.S. Patent No. 4,625,014, to Senter et al.), by hydrolysis of derivatized amino acid side chains (e.g., U.S. Patent No. 4,638,045, to Kohn et al.), by serum complement-mediated hydrolysis (e.g., U.S. Patent No. 4,671,958, to Rodwell et al.), and acid-catalyzed hydrolysis (e.g., U.S. Patent No. 4,569,789, to Blattler et al.).

It may be desirable to couple more than one agent to an antibody. In one embodiment, multiple molecules of an agent are coupled to one antibody molecule. In another embodiment, more than one type of agent may be coupled to one antibody. Regardless of the particular embodiment, immunoconjugates with more than one agent may be prepared in a variety of ways. For example, more than one agent may be coupled directly to an antibody molecule, or linkers which provide multiple sites for attachment can be used. Alternatively, a carrier can be used.

A carrier may bear the agents in a variety of ways, including covalent bonding either directly or via a linker group. Suitable carriers include proteins such as albumins (e.g., U.S. Patent No. 4,507,234, to Kato et al.), peptides and polysaccharides such as aminodextran (e.g., U.S. Patent No. 4,699,784, to Shih et al.). A carrier may also bear an agent by noncovalent bonding or by encapsulation, such as within a liposome vesicle (e.g., U.S. Patent Nos. 4,429,008 and 4,873,088). Carriers specific for radionuclide agents include radiohalogenated small molecules and chelating compounds. For example, U.S. Patent No. 4,735,792 discloses representative radiohalogenated small molecules and their synthesis. A radionuclide chelate may be formed from chelating compounds that include those containing

nitrogen and sulfur atoms as the donor atoms for binding the metal, or metal oxide, radionuclide. For example, U.S. Patent No. 4,673,562, to Davison et al. discloses representative chelating compounds and their synthesis.

A variety of routes of administration for the antibodies and immunoconjugates may be used. Typically, administration will be intravenous, intramuscular, subcutaneous or in the bed of a resected tumor. It will be evident that the precise dose of the antibody/immunoconjugate will vary depending upon the antibody used, the antigen density on the tumor, and the rate of clearance of the antibody.

Diagnostic reagents of the present invention may also comprise DNA sequences encoding one or more of the above polypeptides, or one or more portions thereof. For example, at least two oligonucleotide primers may be employed in a polymerase chain reaction (PCR) based assay to amplify prostate tumor-specific cDNA derived from a biological sample, wherein at least one of the oligonucleotide primers is specific for a DNA molecule encoding a prostate tumor protein of the present invention. The presence of the amplified cDNA is then detected using techniques well known in the art, such as gel electrophoresis. Similarly, oligonucleotide probes specific for a DNA molecule encoding a prostate tumor protein of the present invention may be used in a hybridization assay to detect the presence of an inventive polypeptide in a biological sample.

As used herein, the term "oligonucleotide primer/probe specific for a DNA molecule" means an oligonucleotide sequence that has at least about 80%, preferably at least about 90% and more preferably at least about 95%, identity to the DNA molecule in question. Oligonucleotide primers and/or probes which may be usefully employed in the inventive diagnostic methods preferably have at least about 10-40 nucleotides. In a preferred embodiment, the oligonucleotide primers comprise at least about 10 contiguous nucleotides of a DNA molecule having a sequence selected from SEQ ID NOS: 1-107, 109-111, 115-171, 173-175, 177 and 179-224. Preferably, oligonucleotide probes for use in the inventive diagnostic methods comprise at least about 15 contiguous oligonucleotides of a DNA molecule having a sequence provided in SEQ ID NOS: 1-107, 109-111, 115-171, 173-175, 177 and 179-224. Techniques for both PCR based assays and hybridization assays are well known in the art (see, for example, Mullis *et al. Ibid*; Ehrlich, *Ibid*). Primers or probes may

thus be used to detect prostate tumor-specific sequences in biological samples, including blood, semen, prostate tissue and/or prostate tumor tissue.

The following Examples are offered by way of illustration and not by way of limitation.

EXAMPLES

Example 1

ISOLATION AND CHARACTERIZATION OF PROSTATE TUMOR POLYPEPTIDES

This Example describes the isolation of prostate tumor polypeptides from a prostate tumor cDNA library.

A human prostate tumor cDNA expression library was constructed from prostate tumor poly A⁺ RNA using a Superscript Plasmid System for cDNA Synthesis and Plasmid Cloning kit (BRL Life Technologies, Gaithersburg, MD 20897) following the manufacturer's protocol. Specifically, prostate tumor tissues were homogenized with polytron (Kinematica, Switzerland) and total RNA was extracted using Trizol reagent (BRL Life Technologies) as directed by the manufacturer. The poly A⁺ RNA was then purified using a Qiagen oligotex spin column mRNA purification kit (Qiagen, Santa Clarita, CA 91355) according to the manufacturer's protocol. First-strand cDNA was synthesized using the NotI/Oligo-dT18 primer. Double-stranded cDNA was synthesized, ligated with EcoRI/BAXI adaptors (Invitrogen, San Diego, CA) and digested with NotI. Following size fractionation with Chroma Spin-1000 columns (Clontech, Palo Alto, CA 94303), the cDNA was ligated into the EcoRI/NotI site of pCDNA3.1 (Invitrogen) and transformed into ElectroMax *E. coli* DH10B cells (BRL Life Technologies) by electroporation.

Using the same procedure, a normal human pancreas cDNA expression library was prepared from a pool of six tissue specimens (Clontech). The cDNA libraries were characterized by determining the number of independent colonies, the percentage of clones that carried insert, the average insert size and by sequence analysis. The prostate tumor

library contained 1.64×10^7 independent colonies, with 70% of clones having an insert and the average insert size being 1745 base pairs. The normal pancreas cDNA library contained 3.3×10^6 independent colonies, with 69% of clones having inserts and the average insert size being 1120 base pairs. For both libraries, sequence analysis showed that the majority of clones had a full length cDNA sequence and were synthesized from mRNA, with minimal rRNA and mitochondrial DNA contamination.

cDNA library subtraction was performed using the above prostate tumor and normal pancreas cDNA libraries, as described by Hara *et al.* (*Blood*, 84:189-199, 1994) with some modifications. Specifically, a prostate tumor-specific subtracted cDNA library was generated as follows. Normal pancreas cDNA library (70 µg) was digested with EcoRI, NotI, and SfuI, followed by a filling-in reaction with DNA polymerase Klenow fragment. After phenol-chloroform extraction and ethanol precipitation, the DNA was dissolved in 100 µl of H₂O, heat-denatured and mixed with 100 µl (100 µg) of Photoprobe biotin (Vector Laboratories, Burlingame, CA). As recommended by the manufacturer, the resulting mixture was irradiated with a 270 W sunlamp on ice for 20 minutes. Additional Photoprobe biotin (50 µl) was added and the biotinylation reaction was repeated. After extraction with butanol five times, the DNA was ethanol-precipitated and dissolved in 23 µl H₂O to form the driver DNA.

To form the tracer DNA, 10 µg prostate tumor cDNA library was digested with BamHI and XhoI, phenol chloroform extracted and passed through Chroma spin-400 columns (Clontech). Following ethanol precipitation, the tracer DNA was dissolved in 5 µl H₂O. Tracer DNA was mixed with 15 µl driver DNA and 20 µl of 2 x hybridization buffer (1.5 M NaCl/10 mM EDTA/50 mM HEPES pH 7.5/0.2% sodium dodecyl sulfate), overlaid with mineral oil, and heat-denatured completely. The sample was immediately transferred into a 68 °C water bath and incubated for 20 hours (long hybridization [LH]). The reaction mixture was then subjected to a streptavidin treatment followed by phenol/chloroform extraction. This process was repeated three more times. Subtracted DNA was precipitated, dissolved in 12 µl H₂O, mixed with 8 µl driver DNA and 20 µl of 2 x hybridization buffer, and subjected to a hybridization at 68 °C for 2 hours (short hybridization [SH]). After removal of biotinylated double-stranded DNA, subtracted cDNA was ligated into

BamHI/XbaI site of chloramphenicol resistant pBCSK⁺ (Stratagene, La Jolla, CA 92037) and transformed into ElectroMax *E. coli* DH10B cells by electroporation to generate a prostate tumor specific subtracted cDNA library (prostate subtraction 1).

To analyze the subtracted cDNA library, plasmid DNA was prepared from 100 independent clones, randomly picked from the subtracted prostate tumor specific library and grouped based on insert size. Representative cDNA clones were further characterized by DNA sequencing with a Perkin Elmer/Applied Biosystems Division Automated Sequencer Model 373A (Foster City, CA). Six cDNA clones, hereinafter referred to as F1-13, F1-12, F1-16, H1-1, H1-9 and H1-4, were shown to be abundant in the subtracted prostate-specific cDNA library. The determined 3' and 5' cDNA sequences for F1-12 are provided in SEQ ID NO: 2 and 3, respectively, with determined 3' cDNA sequences for F1-13, F1-16, H1-1, H1-9 and H1-4 being provided in SEQ ID NO: 1 and 4-7, respectively.

The cDNA sequences for the isolated clones were compared to known sequences in the gene bank using the EMBL and GenBank databases (release 96). Four of the prostate tumor cDNA clones, F1-13, F1-16, H1-1, and H1-4, were determined to encode the following previously identified proteins: prostate specific antigen (PSA), human glandular kallikrein, human tumor expression enhanced gene, and mitochondria cytochrome C oxidase subunit II. H1-9 was found to be identical to a previously identified human autonomously replicating sequence. No significant homologies to the cDNA sequence for F1-12 were found.

Subsequent studies led to the isolation of a full-length cDNA sequence for F1-12. This sequence is provided in SEQ ID NO: 107, with the corresponding predicted amino acid sequence being provided in SEQ ID NO: 108.

To clone less abundant prostate tumor specific genes, cDNA library subtraction was performed by subtracting the prostate tumor cDNA library described above with the normal pancreas cDNA library and with the three most abundant genes in the previously subtracted prostate tumor specific cDNA library: human glandular kallikrein, prostate specific antigen (PSA), and mitochondria cytochrome C oxidase subunit II. Specifically, 1 µg each of human glandular kallikrein, PSA and mitochondria cytochrome C oxidase subunit II cDNAs in pCDNA3.1 were added to the driver DNA and subtraction was

performed as described above to provide a second subtracted cDNA library hereinafter referred to as the "subtracted prostate tumor specific cDNA library with spike".

Twenty-two cDNA clones were isolated from the subtracted prostate tumor specific cDNA library with spike. The determined 3' and 5' cDNA sequences for the clones referred to as J1-17, L1-12, N1-1862, J1-13, J1-19, J1-25, J1-24, K1-58, K1-63, L1-4 and L1-14 are provided in SEQ ID NOS: 8-9, 10-11, 12-13, 14-15, 16-17, 18-19, 20-21, 22-23, 24-25, 26-27 and 28-29, respectively. The determined 3' cDNA sequences for the clones referred to as J1-12, J1-16, J1-21, K1-48, K1-55, L1-2, L1-6, N1-1858, N1-1860, N1-1861, N1-1864 are provided in SEQ ID NOS: 30-40, respectively. Comparison of these sequences with those in the gene bank as described above, revealed no significant homologies to three of the five most abundant DNA species, (J1-17, L1-12 and N1-1862; SEQ ID NOS: 8-9, 10-11 and 12-13, respectively). Of the remaining two most abundant species, one (J1-12; SEQ ID NO:30) was found to be identical to the previously identified human pulmonary surfactant-associated protein, and the other (K1-48; SEQ ID NO:33) was determined to have some homology to *R. norvegicus* mRNA for 2-arylpropionyl-CoA epimerase. Of the 17 less abundant cDNA clones isolated from the subtracted prostate tumor specific cDNA library with spike, four (J1-16, K1-55, L1-6 and N1-1864; SEQ ID NOS:31, 34, 36 and 40, respectively) were found to be identical to previously identified sequences, two (J1-21 and N1-1860; SEQ ID NOS: 32 and 38, respectively) were found to show some homology to non-human sequences, and two (L1-2 and N1-1861; SEQ ID NOS: 35 and 39, respectively) were found to show some homology to known human sequences. No significant homologies were found to the polypeptides J1-13, J1-19, J1-24, J1-25, K1-58, K1-63, L1-4, L1-14 (SEQ ID NOS: 14-15, 16-17, 20-21, 18-19, 22-23, 24-25, 26-27, 28-29, respectively).

Subsequent studies led to the isolation of full length cDNA sequences for J1-17, L1-12 and N1-1862 (SEQ ID NOS: 109-111, respectively). The corresponding predicted amino acid sequences are provided in SEQ ID NOS: 112-114.

In a further experiment, four additional clones were identified by subtracting a prostate tumor cDNA library with normal prostate cDNA prepared from a pool of three normal prostate poly A+ RNA (prostate subtraction 2). The determined cDNA sequences for these clones, hereinafter referred to as U1-3064, U1-3065, V1-3692 and 1A-3905, are

provided in SEQ ID NO: 69-72, respectively. Comparison of the determined sequences with those in the gene bank revealed no significant homologies to U1-3065.

A second subtraction with spike (prostate subtraction spike 2) was performed by subtracting a prostate tumor specific cDNA library with spike with normal pancreas cDNA library and further spiked with PSA, J1-17, pulmonary surfactant-associated protein, mitochondrial DNA, cytochrome c oxidase subunit II, N1-1862, autonomously replicating sequence, L1-12 and tumor expression enhanced gene. Four additional clones, hereinafter referred to as V1-3686, R1-2330, 1B-3976 and V1-3679, were isolated. The determined cDNA sequences for these clones are provided in SEQ ID NO:73-76, respectively. Comparison of these sequences with those in the gene bank revealed no significant homologies to V1-3686 and R1-2330.

Further analysis of the three prostate subtractions described above (prostate subtraction 2, subtracted prostate tumor specific cDNA library with spike, and prostate subtraction spike 2) resulted in the identification of sixteen additional clones, referred to as 1G-4736, 1G-4738, 1G-4741, 1G-4744, 1G-4734, 1H-4774, 1H-4781, 1H-4785, 1H-4787, 1H-4796, 1I-4810, 1I-4811, 1J-4876, 1K-4884 and 1K-4896. The determined cDNA sequences for these clones are provided in SEQ ID NOS: 77-92, respectively. Comparison of these sequences with those in the gene bank as described above, revealed no significant homologies to 1G-4741, 1G-4734, 1I-4807, 1J-4876 and 1K-4896 (SEQ ID NOS: 79, 81, 87, 90 and 92, respectively). Further analysis of the isolated clones led to the determination of extended cDNA sequences for 1G-4736, 1G-4738, 1G-4741, 1G-4744, 1H-4774, 1H-4781, 1H-4785, 1H-4787, 1H-4796, 1I-4807, 1J-4876, 1K-4884 and 1K-4896, provided in SEQ ID NOS: 179-188 and 191-193, respectively, and to the determination of additional partial cDNA sequences for 1I-4810 and 1I-4811, provided in SEQ ID NOS: 189 and 190, respectively.

An additional subtraction was performed by subtracting a normal prostate cDNA library with normal pancreas cDNA (prostate subtraction 3). This led to the identification of six additional clones referred to as 1G-4761, 1G-4762, 1H-4766, 1H-4770, 1H-4771 and 1H-4772 (SEQ ID NOS: 93-98). Comparison of these sequences with those in the gene bank revealed no significant homologies to 1G-4761 and 1H-4771 (SEQ ID NOS:

93 and 97, respectively). Further analysis of the isolated clones led to the determination of extended cDNA sequences for 1G-4761, 1G-4762, 1H-4766 and 1H-4772 provided in SEQ ID NOS: 194-196 and 199, respectively, and to the determination of additional partial cDNA sequences for 1H-4770 and 1H-4771, provided in SEQ ID NOS: 197 and 198, respectively.

Subtraction of a prostate tumor cDNA library, prepared from a pool of polyA+ RNA from three prostate cancer patients, with a normal pancreas cDNA library (prostate subtraction 4) led to the identification of eight clones, referred to as 1D-4297, 1D-4309, 1D.1-4278, 1D-4288, 1D-4283, 1D-4304, 1D-4296 and 1D-4280 (SEQ ID NOS: 99-107). These sequences were compared to those in the gene bank as described above. No significant homologies were found to 1D-4283 and 1D-4304 (SEQ ID NOS: 103 and 104, respectively). Further analysis of the isolated clones led to the determination of extended cDNA sequences for 1D-4309, 1D.1-4278, 1D-4288, 1D-4283, 1D-4304, 1D-4296 and 1D-4280, provided in SEQ ID NOS: 200-206, respectively. cDNA clones isolated in prostate subtraction 1 and prostate subtraction 2, described above, were colony PCR amplified and their mRNA expression levels in prostate tumor, normal prostate and in various other normal tissues were determined using microarray technology (Synteni, Palo Alto, CA). Briefly, the PCR amplification products were dotted onto slides in an array format, with each product occupying a unique location in the array. mRNA was extracted from the tissue sample to be tested, reverse transcribed, and fluorescent-labeled cDNA probes were generated. The microarrays were probed with the labeled cDNA probes, the slides scanned and fluorescence intensity was measured. This intensity correlates with the hybridization intensity. Two novel clones (referred to as P509S and P510S) were found to be over-expressed in prostate tumor and normal prostate and expressed at low levels in all other normal tissues tested (liver, pancreas, skin, bone marrow, brain, breast, adrenal gland, bladder, testes, salivary gland; large intestine, kidney, ovary, lung, spinal cord, skeletal muscle and colon). The determined cDNA sequences for P509S and P510S are provided in SEQ ID NO: 223 and 224, respectively. Comparison of these sequences with those in the gene bank as described above, revealed some homology to previously identified ESTs.

Example 2**DETERMINATION OF TISSUE SPECIFICITY OF PROSTATE TUMOR
POLYPEPTIDES**

Using gene specific primers, mRNA expression levels for the representative prostate tumor polypeptides F1-16, H1-1, J1-17, L1-12, F1-12 and N1-1862 were examined in a variety of normal and tumor tissues using RT-PCR.

Briefly, total RNA was extracted from a variety of normal and tumor tissues using Trizol reagent as described above. First strand synthesis was carried out using 1-2 µg of total RNA with SuperScript II reverse transcriptase (BRL Life Technologies) at 42 °C for one hour. The cDNA was then amplified by PCR with gene-specific primers. To ensure the semi-quantitative nature of the RT-PCR, β-actin was used as an internal control for each of the tissues examined. First, serial dilutions of the first strand cDNAs were prepared and RT-PCR assays were performed using β-actin specific primers. A dilution was then chosen that enabled the linear range amplification of the β-actin template and which was sensitive enough to reflect the differences in the initial copy numbers. Using these conditions, the β-actin levels were determined for each reverse transcription reaction from each tissue. DNA contamination was minimized by DNase treatment and by assuring a negative PCR result when using first strand cDNA that was prepared without adding reverse transcriptase.

mRNA Expression levels were examined in four different types of tumor tissue (prostate tumor from 2 patients, breast tumor from 3 patients, colon tumor, lung tumor), and sixteen different normal tissues, including prostate, colon, kidney, liver, lung, ovary, pancreas, skeletal muscle, skin, stomach, testes, bone marrow and brain. F1-16 was found to be expressed at high levels in prostate tumor tissue, colon tumor and normal prostate, and at lower levels in normal liver, skin and testes, with expression being undetectable in the other tissues examined. H1-1 was found to be expressed at high levels in prostate tumor, lung tumor, breast tumor, normal prostate, normal colon and normal brain, at much lower levels in normal lung, pancreas, skeletal muscle, skin, small intestine, bone marrow, and was not detected in the other tissues tested. J1-17 and L1-12 appear to be specifically over-expressed in prostate, with both genes being expressed at high levels in

prostate tumor and normal prostate but at low to undetectable levels in all the other tissues examined. N1-1862 was found to be over-expressed in 60% of prostate tumors and detectable in normal colon and kidney. The RT-PCR results thus indicate that F1-16, H1-1, J1-17, N1-1862 and L1-12 are either prostate specific or are expressed at significantly elevated levels in prostate.

Further RT-PCR studies showed that F1-12 is over-expressed in 60% of prostate tumors, detectable in normal kidney but not detectable in all other tissues tested. Similarly, R1-2330 was shown to be over-expressed in 40% of prostate tumors, detectable in normal kidney and liver, but not detectable in all other tissues tested. U1-3064 was found to be over-expressed in 60% of prostate tumors, and also expressed in breast and colon tumors, but was not detectable in normal tissues.

RT-PCR characterization of R1-2330, U1-3064 and 1D-4279 showed that these three antigens are over-expressed in prostate and/or prostate tumors.

Northern analysis with four prostate tumors, two normal prostate samples, two BPH prostates, and normal colon, kidney, liver, lung, pancreas, skeletal muscle, brain, stomach, testes, small intestine and bone marrow, showed that L1-12 is over-expressed in prostate tumors and normal prostate, while being undetectable in other normal tissues tested. J1-17 was detected in two prostate tumors and not in the other tissues tested. N1-1862 was found to be over-expressed in three prostate tumors and to be expressed in normal prostate, colon and kidney, but not in other tissues tested. F1-12 was found to be highly expressed in two prostate tumors and to be undetectable in all other tissues tested.

The micro-array technology described above was used to determine the expression levels of representative antigens described herein in prostate tumor, breast tumor and the following normal tissues: prostate, liver, pancreas, skin, bone marrow, brain, breast, adrenal gland, bladder, testes, salivary gland, large intestine, kidney, ovary, lung, spinal cord, skeletal muscle and colon. L1-12 was found to be over-expressed in normal prostate and prostate tumor, with some expression being detected in normal skeletal muscle. Both J1-12 and F1-12 were found to be over-expressed in prostate tumor, with expression being lower or undetectable in all other tissues tested. N1-1862 was found to be expressed at high levels in prostate tumor and normal prostate, and at low levels in normal large intestine and normal

colon, with expression being undetectable in all other tissues tested. R1-2330 was found to be over-expressed in prostate tumor and normal prostate, and to be expressed at lower levels in all other tissues tested. 1D-4279 was found to be over-expressed in prostate tumor and normal prostate, expressed at lower levels in normal spinal cord, and to be undetectable in all other tissues tested.

Example 3

ISOLATION AND CHARACTERIZATION OF PROSTATE TUMOR POLYPEPTIDES BY PCR-BASED SUBTRACTION

A cDNA subtraction library, containing cDNA from normal prostate subtracted with ten other normal tissue cDNAs (brain, heart, kidney, liver, lung, ovary, placenta, skeletal muscle, spleen and thymus) and then submitted to a first round of PCR amplification, was purchased from Clontech. This library was subjected to a second round of PCR amplification, following the manufacturer's protocol. The resulting cDNA fragments were subcloned into the vector pT7 Blue T-vector (Novagen, Madison, WI) and transformed into XL-1 Blue MRF' *E. coli* (Stratagene). DNA was isolated from independent clones and sequenced using a Perkin Elmer/Applied Biosystems Division Automated Sequencer Model 373A.

Fifty-nine positive clones were sequenced. Comparison of the DNA sequences of these clones with those in the gene bank, as described above, revealed no significant homologies to 25 of these clones, hereinafter referred to as P5, P8, P9, P18, P20, P30, P34, P36, P38, P39, P42, P49, P50, P53, P55, P60, P64, P65, P73, P75, P76, P79 and P84. The determined cDNA sequences for these clones are provided in SEQ ID NO:41-45, 47-52 and 54-65, respectively. P29, P47, P68, P80 and P82 (SEQ ID NO:46, 53 and 66-68, respectively) were found to show some degree of homology to previously identified DNA sequences. To the best of the inventors' knowledge, none of these sequences have been previously shown to be present in prostate.

Further studies using the PCR-based methodology described above resulted in the isolation of more than 180 additional clones, of which 23 clones were found to show no

significant homologies to known sequences. The determined cDNA sequences for these clones are provided in SEQ ID NO: 115-123, 127, 131, 137, 145, 147-151, 153, 156-158 and 160. Twenty-three clones (SEQ ID NO: 124-126, 128-130, 132-136, 138-144, 146, 152, 154, 155 and 159) were found to show some homology to previously identified ESTs. An additional ten clones (SEQ ID NO: 161-170) were found to have some degree of homology to known genes. An additional clone, referred to as P703, was found to have five splice variants. The determined DNA sequence for the variants referred to as DE1, DE13 and DE14 are provided in SEQ ID NOS: 171, 175 and 177, respectively, with the corresponding predicted amino acid sequences being provided in SEQ ID NO: 172, 176 and 178, respectively. The DNA sequences for the splice variants referred to as DE2 and DE6 are provided in SEQ ID NOS: 173 and 174, respectively.

mRNA Expression levels for representative clones in tumor tissues (prostate (n=5), breast (n=2), colon and lung) normal tissues (prostate (n=5), colon, kidney, liver, lung (n=2), ovary (n=2), skeletal muscle, skin, stomach, small intestine and brain), and activated and non-activated PBMC was determined by RT-PCT as described above. Expression was examined in one sample of each tissue type unless otherwise indicated.

P9 was found to be highly expressed in normal prostate and prostate tumor compared to all normal tissues tested except for normal colon which showed comparable expression. P20 was found to be highly expressed in normal prostate and prostate tumor, compared to all twelve normal tissues tested. A modest increase in expression of P20 in breast tumor (n=2), colon tumor and lung tumor was seen compared to all normal tissues except lung (1 of 2). Increased expression of P18 was found in normal prostate, prostate tumor and breast tumor compared to other normal tissues except lung and stomach. A modest increase in expression of P5 was observed in normal prostate compared to most other normal tissues. However, some elevated expression was seen in normal lung and PBMC. Elevated expression of P5 was also observed in prostate tumors (2 of 5), breast tumor and one lung tumor sample. For P30, similar expression levels were seen in normal prostate and prostate tumor, compared to six of twelve other normal tissues tested. Increased expression was seen in breast tumors, one lung tumor sample and one colon tumor sample, and also in normal PBMC. P29 was found to be over-expressed in prostate tumor (5 of 5) and normal prostate (5

of 5) compared to the majority of normal tissues. However, substantial expression of P29 was observed in normal colon and normal lung (2 of 2). P80 was found to be over-expressed in prostate tumor (5 of 5) and normal prostate (5 of 5) compared to all other normal tissues tested, with increased expression also being seen in colon tumor.

Further studies using the above methodology resulted in the isolation of twelve additional clones, hereinafter referred to as 10-d8, 10-h10, 11-c8, 7-g6, 8-b5, 8-b6, 8-d4, 8-d9, 8-g3, 8-h11, g-f12 and g-f3. The determined DNA sequences for 10-d8, 10-h10, 11-c8, 8-d4, 8-d9, 8-h11, g-f12 and g-f3 are provided in SEQ ID NO: 207, 208, 209, 216, 217, 220, 221 and 222, respectively. The determined forward and reverse DNA sequences for 7-g6, 8-b5, 8-b6 and 8-g3 are provided in SEQ ID NO: 210 and 211; 212 and 213; 214 and 215; and 218 and 219, respectively. Comparison of these sequences with those in the gene bank revealed no significant homologies to the sequences of 7-g6 and g-f3. The clones 10-d8, 11-c8 and 8-h11 were found to show some homology to previously isolated ESTs, while 10-h10, 8-b5, 8-b6, 8-d4, 8-d9, 8-g3 and g-f12 were found to show some homology to previously identified genes.

Example 4

SYNTHESIS OF POLYPEPTIDES

Polypeptides may be synthesized on a Perkin Elmer/Applied Biosystems 430A peptide synthesizer using Fmoc chemistry with HPTU (O-Benzotriazole-N,N,N',N'-tetramethyluronium hexafluorophosphate) activation. A Gly-Cys-Gly sequence may be attached to the amino terminus of the peptide to provide a method of conjugation, binding to an immobilized surface, or labeling of the peptide. Cleavage of the peptides from the solid support may be carried out using the following cleavage mixture: trifluoroacetic acid:ethanedithiol:thioanisole:water:phenol (40:1:2:2:3). After cleaving for 2 hours, the peptides may be precipitated in cold methyl-t-butyl-ether. The peptide pellets may then be dissolved in water containing 0.1% trifluoroacetic acid (TFA) and lyophilized prior to purification by C18 reverse phase HPLC. A gradient of 0%-60% acetonitrile (containing 0.1% TFA) in water (containing 0.1% TFA) may be used to elute the peptides. Following

lyophilization of the pure fractions, the peptides may be characterized using electrospray or other types of mass spectrometry and by amino acid analysis.

From the foregoing, it will be appreciated that, although specific embodiments of the invention have been described herein for the purposes of illustration, various modifications may be made without deviating from the spirit and scope of the invention.

SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANTS: Xu, Jiangchun
Dillin, Davin C.

(ii) TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY OF PROSTATE CANCER
AND METHODS FOR THEIR USE

(iii) NUMBER OF SEQUENCES: 224

(iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: SEED and BERRY LLP
(B) STREET: 6300 Columbia Center, 701 Fifth Avenue
(C) CITY: Seattle
(D) STATE: WA
(E) COUNTRY: USA
(F) ZIP: 98104

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: PatentIn Release #1.0, Version #1.30

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER:
(B) FILING DATE: 23-FEB-1998
(C) CLASSIFICATION:

(viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: Maki, David J.
(B) REGISTRATION NUMBER: 31,392
(C) REFERENCE/DOCKET NUMBER: 210121.427C3

(ix) TELECOMMUNICATION INFORMATION:

(A) TELEPHONE: (206) 622-4900
(B) TELEFAX: (206) 682-6031

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 814 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

| | | | | | | |
|------------|------------|------------|------------|------------|-------------|-----|
| TTTTTTTTTT | TTTTTCACAG | TATAACAGCT | CTTTATTCT | GTGAGTCTA | CTAGGAAATC | 60 |
| ATCAAATCTG | AGGGTTGTCT | GGAGGACTTC | AATACACCTC | CCCCCATAGT | GAATCAGCTT | 120 |
| CCAGGGGGTC | CAGTCCTCT | CCTTACTTCA | TCCCCATCCC | ATGCCAAAGG | AAGACCCCTCC | 180 |
| CTCCTTGCGT | CACAGCCTTC | TCTAGGCTTC | CCAGTGCTC | CAGGACAGAG | TGGGTTATGT | 240 |
| TTTCAGCTCC | ATCCTTGCTG | TGAGTGCTG | GTGCGTTGTG | CCTCCAGCTT | CTGCTCAGTG | 300 |
| CTTCATGGAC | AGTGTCCAGC | ACATGTCACT | CTCCACTCTC | TCAGTGTGGA | TCCACTAGTT | 360 |
| CTAGAGCGGC | CGCCACCGCG | GTGGAGCTCC | AGCTTTGTT | CCCTTTAGTG | AGGGTTAATT | 420 |

| | |
|----------------------------------|-----|
| GCGCGCTTGG CGTAATCATG GTCATAACTG | 480 |
| TTTCCTGTGT GAAATTGTTA TCCGCTACA | |
| ATCCACACA ACATACGAGC CGGAAGCATA | 540 |
| AAGTGTAAG CCTGGGGTGC CTAATGAGTG | |
| ANCTAACTCA CATTAATTGC GTTGCGCTCA | 600 |
| CTGNCCGCTT TCCAGTCNGG AAAACTGTCG | |
| TGCCAGCTGC ATTAATGAAT CGGCCAACCG | 660 |
| NCGGGGAAA GCGGTTTGCCT TTTGGGGGC | |
| TCTTCCGCTT CTCGCTCACT NANTCCTGCG | 720 |
| CTCGTCNTT CGGCTGCNGG GAACGGTATC | |
| ACTCCTAAA GGNGTATTAA CGGTTATCCN | 780 |
| NAAATCNGGG GATACCCNGG AAAAAANTTT | |
| AACAAAGGG CANCAAAGGG CNGAAACGTA | 814 |
| AAAA | |

(2) INFORMATION FOR SEQ ID NO:2:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 816 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

| | |
|---|-----|
| ACAGAAATGT TGGATGGTGG AGCACCTTTC | 60 |
| TATACGACTT ACAGGACAGC AGATGGGGAA | |
| TTCATGGCTG TTGGAGCAAT AGAACCCCAG | 120 |
| TTCTACGAGC TGCTGATCAA AGGACTTGGA | |
| CTAAAGTCTG ATGAACCTTC CAATCAGATG | 180 |
| AGCATGGATG ATTGGCCAGA AATGAAGAAG | |
| AAGTTTGAG ATGTATTGCA AAAGAAAGACG | 240 |
| AAGGCAGAGT GTGTCAGAAT CTGGACGGC | |
| ACAGATGCCT GTGTGACTCC GGTTCTGACT | 300 |
| TTTGAGGAGG TTGTTCATCA TGATCACAAAC | |
| AAGGAACGGG GCTCGTTAT CACCAGTGAG | 360 |
| GAGCAGGACG TGAGCCCCCG CCCTGCACCT | |
| CTGCTGTTAA ACACCCACG CATCCCTCT | 420 |
| TTCAAAAGGG ATCCACTAGT TCTAGAAGCG | |
| GCCGCCACCG CGGTGGAGCT CCAGCTTTG | 480 |
| TTCCCTTAG TGAGGGTTAA TTGCGCGCTT | |
| GGCGTAATCA TGGTCATAGC TGTTCTGT | 540 |
| GTGAAATTGT TATCCGCTCA CAATTCCCCC | |
| AACATACGAG CGCGAACATA AAGTGTAAAG | 600 |
| CCTGGGGTGC CTAATGANTG AGCTAACTCN | |
| CATTAATTGC GTTGCGCTCA CTGCCCCCTT | 660 |
| TCCAGTCGGG AAAACTGTCG TGCCACTGCN | |
| TTANTGAATC NGCCACCCCC CGGGAAAAGG | 720 |
| CGGTGTCNTT TTGGGCCTCT TCCGCTTCC | |
| TCGCTCATTC ATCCTNGCNC CGGGCTTCG | 780 |
| GCTGGGGNGA ACCGTTCACT CCTCAAAGGC | |
| GGTNNTNCGG TTATCCCCAA ACNGGGGATA CCCNGA | 816 |

(2) INFORMATION FOR SEQ ID NO:3:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 773 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

| | |
|--|-----|
| CTTTGAAAG AAGGGATGGC TGGGGTGTAA AACAGCAGAG GTGCAGGGCG | 60 |
| GGGGCTCACG | |
| TCCTGCTCCT CACTGGTGAT AAACGAGCCC CGTCTCTGT TGATGATCATG | 120 |
| ATGAACAAAC | |
| TCCTAAAGA TCAGAACCGG AGTCACACAG GCATCTGTGC | 180 |
| CGTCAAAGAT TTGACACCAC | |
| TCTGCCCTCG TCTTCTTGC AAATACATCT GCAAACCTCT | 240 |
| TCTTCATITC TGGCCAATCA | |
| TCCATGCTCA TCTGATTGGG AAGTTCATCA GACTTTAGTC | 300 |
| CANNCTCTTT GATCAGCAGC | |
| TCCCTAGAACT GGGGTTCTAT TGCTCCAAAC | 360 |
| GCCATGAATT CCCCATCTGC TGCCCTGTAA | |
| GTCTGATAGA AAGGTGCTCC ACCATCCAAC | 420 |
| ATGTTCTGTC CTCGAGGGGG GGCCCCGGTAC | |
| CCAATTCGCC CTATANTGAG TCGTATTACG CGCGCTCACT | 480 |
| GGCCGTCGTT TTACAACGTC | |
| GTGACTGGGA AAACCTGGG CGTTACCAAC TTAATGCGCT | 540 |
| TGCAGCACAT CCCCCCTTCG | |
| CCAGCTGGGC GTAATANCGA AAAGGGCCGC ACCGATGCCC | 600 |
| CTTCCAACAG TTGCGCACCT | |
| GAATGGNAA ATGGGACCCC CCTGTTACCG CGCATTAAC | 660 |
| CCCCGCNGGG TTTNGTTGTT | |
| ACCCCCACNT NNACCGCTTA CACTTGTCCA GCGCCTTANC | 720 |
| CCCCGCTCCC TTTCNCCTTT | |
| CTTCCCTTCC TTTCNCNCNN CTTTCCCCCG GGGTTCCCC CNTCAAACCC | 773 |
| CNA | |

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 828 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

| | |
|--|-----|
| CCTCCTGAGT CCTACTGACC TGTGTTCT GGTGTGGAGT CCAGGGCTGC TAGGAAAAGG | 60 |
| AATGGCAGA CACAGGTGTA TGCCAATGTT TCTGAAATGG GTATAATTTC GTCCCTCTCCT | 120 |
| TCGGAACACT GGCTGTCTCT GAAGACTCT CGCTCAGTTT CAGTGGAGAC ACACACAAAG | 180 |
| ACCTCGGTGA CCATGTTGTT TGTGGGGTGC AGAGATGGGA GGGGTGGGGC CCACCCCTGGA | 240 |
| AGAGTGGACA GTGACACAAG GTGGACACTC TCTACAGATC ACTGAGGATA AGCTGGAGCC | 300 |
| ACAATGCATG AGGCACACAC ACAGCAAGGA TGACNCTGTA AACATAGCCC ACGCTGTCT | 360 |
| GNGGGCACTG GGAAGCCTAN ATNAGGCCGT GAGCANAAAG AAGGGGAGGA TCCACTAGTT | 420 |
| CTANAGCGGC CGCCACCGCG GTGGANCCTC ANCTTTGTT CCCTTTAGTG AGGGTTAACATT | 480 |
| GCGCGCTTGG CNTAACATCG GTCATACNTN TTTCCTGTGT GAAATTGTTA TCCGCTCACAA | 540 |
| ATTCACACACA ACATACGANC CGGAAACATA AANTGTAAC CTGGGGTGCC TAATGANTGA | 600 |
| CTAACTCACA TTAATTGCGT TGCGCTCACT GCCCCCTTTC CAATCNGGAA ACCTGTCITG | 660 |
| CCNCTTGAT TNATGAATCN GCCAACCCCC GGGGAAAGC GTTGCGTTT TGGGCGCTCT | 720 |
| TCCGCTTCT CNCTCANTTA NTCCCTNCNC TCGGTCAATT CGGCTGCNGC AAACCGGTT | 780 |
| ACCNCTCCA AAGGGGTAT TCCGGTTTCC CCNAATCCGG GGANANCC | 828 |

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 834 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

| | |
|---|-----|
| TTTTTTTTTT TTTTTACTGA TAGATGGAAT TTATTAAGCT TTTCACATGT GATAGCACAT | 60 |
| AGTTTTAATT GCATCCAAAG TACTAACAAA AACTCTAGCA ATCAAGAACG GCAGCATGTT | 120 |
| ATTTTATAAC AATCAACACC TGTGGCTTTT AAAATTGGT TTTCATAAGA TAATTTATAC | 180 |
| TGAAAGTAAAT CTAGCCATGC TTTAAAAAAA TGCTTGTAGGT CACTCCAAGC TTGGCAGTTA | 240 |
| ACATTGGCA TAAACAAATAA TAAAACAATC ACAATTAAAT AAAAACACAA TACAACATG | 300 |
| TAGGCCATAA TCATATACAG TATAAGAAA AGGTGGTAGT GTTGAGTAAG CAGTTATTAG | 360 |
| AATAGAATAAC CTTGGCCTCT ATGCAAATAT GTCTAGACAC TTGATTCAAC TCAGCCCTGA | 420 |
| CATTCAAGTT TCAAAGTAGG AGACAGGTT TACAGTATCA TTTTACAGTT TCCAACACAT | 480 |
| TGAAAACAAG TAGAAAATGA TGAGTTGATT TTTATTAATG CATTACATCC TCAAGAGTTA | 540 |
| TCACCAACCC CTCAGTTATA AAAAATTTC AAGTTATATT AGTCATATAA CTTGGGTGTC | 600 |
| TTATTTAAA TTAGTGCTAA ATGGATTAAG TGAAGACAAC AATGGTCCCC TAATGTGATT | 660 |
| GATATTGGTC ATTTTACCA GCTTCTAAAT CTNAACTTTC AGGCTTTGA ACTGGAACAT | 720 |
| TGNATNACAG TGTCCANAG TTNCAACCTA CTGGAACATT ACAGTGTGCT TGATTCAAAA | 780 |
| TGTTATTTTG TTAAGGTTAACC TGGTGGAAAA ATAATTTGAA ATNA | 834 |

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 818 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

| | |
|---|-----|
| TTTTTTTTT TTTTTTTTTT AAGACCCTCA TCAATAGATG GAGACATACA GAAATAGTCA | 60 |
| AACCACATCT ACAAAATGCC AGTATCAGGC GGCGGCTTCG AAGCCAAAGT GATGTTTGGA | 120 |
| TGTAAAGTGA AATATTAGTT GGCGGATGAA GCAGATAGTG AGGAAAGTTG AGCCAATAAT | 180 |
| GACGTGAAGT CCGTGGAAAGC CTGTGGCTAC AAAAATGTT GAGCCGTAGA TGCCGTCGGA | 240 |
| AATGGTGAAG GGAGACTCGA AGTACTCTGA GGCTGTAGG AGGGTAAAT AGAGACCCAG | 300 |
| TAAAATTGTA ATAAGCAGTG CTTGAATAT TTGTTTTCGG TTGTTTCTA TTAGACTATG | 360 |
| GTGAGCTCAG GTGATTGATA CTCTGTATGC GAGTAATACG GATGTGTTA GGAGTGGGAC | 420 |
| TTCTAGGGGA TTAGCGGGG TGATGCCGTG TGGGGCCAG TGCCCTCCTA GTGGGGGGT | 480 |
| AGGGGCTAGG CTGGAGTGGT AAAAGGCTCA GAAAATCCT GCGAAGAAAA AAACCTCTGA | 540 |
| GGTAATAAT AGGATTATCC CGTATCGAAG GCCTTTTGG ACAGGTGGTG TGTGGTGGCC | 600 |
| TTGGTATGTG CTTTCTCGT TTACATCGCG CCATCATTGG TATATGGTTA GTGTGTTGG | 660 |
| TTANTANGGC CTANTATGAA GAACTTTGG ANTGGAATTA AATCAATNGC TTGGCCGGAA | 720 |
| GTCATTANGA NGGCTNAAA GGCCCTGTTA NGGGTCTGGG CTNGTTTA CCCNACCCAT | 780 |
| GGAATNCNCC CCCCGGACNA NTGNATCCCT ATTCTTAA | 818 |

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 817 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

| | |
|--|-----|
| TTTTTTTTT TTTTTTTTTT TGGCTCTAGA GGGGGTAGAG GGGGTGCTAT AGGGTAAATA | 60 |
| CGGGCCCTAT TTCAAAGATT TTAGGGGAA TTAATTCTAG GACGATGGGT ATGAAACTGT | 120 |
| GGTTTGCTCC ACAGATTTCAG GAGCATGAC CGTAGTATAC CCCCGGTCGT GTAGCGGTGA | 180 |
| AAGTGGTTTG GTTAGACGT CGGGGAATTG CATCTGTTT TAAGCCTAAT GTGGGGACAG | 240 |
| CTCATGAGTG CAAGACGCTC TGTGATGTA TTATTATACN AATGGGGGCT TCAATCGGGA | 300 |
| GTACTACTCG ATTGTCAACG TCAAGGAGTC GCAGGTCGCC TGGTTCTAGG AATAATGGGG | 360 |
| GAAGTATGTA GGAATTGAAG ATTAATCCGC CGTAGTCGGT GTTCTCCTAG GTCAATACC | 420 |
| ATTGGTGGCC AATTGATTG ATGGTAAGGG GAGGGATCGT TGAACTCGTC TGTATGTA | 480 |
| AGGATNCCTT NGGGATGGGA AGGCNATNAA GGACTANGGA TNAATGGCGG GCANGATATT | 540 |
| TCAAACNGTC TCTANTTCCT GAAACGTCG AAATGTTAAT AANAATTAAN TTNGTTATT | 600 |
| GAATNTTNNG GAAAAGGGCT TACAGGACTA GAAACCAAAT ANGAAAANTA ATNNNTAANGG | 660 |
| CNTTATCNNT AAAGGTNATA ACCNCTCTA TNATCCCACC CAATNGNATT CCCCACNCNN | 720 |
| ACNATTGGAT NCNCANTTC CANAAANGGC CNCCCCCGG TGNANNCCNC CTTTTGTTCC | 780 |
| CTTNANTGAN GGTTATTNCNCCCTNGCNNTT ATCANCC | 817 |

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 799 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

| | |
|---|-----|
| CATTTCCGGG TTTACTTTCT AAGGAAAGCC GAGCGGAAGC TGCTAACGTG GGAATCGGTG | 60 |
| CATAAGGAGA ACTTTCTGCT GGCACGCGCT AGGGACAAGC GGGAGAGCGA CTCCGAGCGT | 120 |

| | | | | | | |
|------------|------------|------------|------------|------------|-------------|-----|
| CTGAAGCGCA | CGTCCCAGAA | GGTGGACTTG | GCACTGAAAC | AGCTGGGACA | CATCCGCGAG | 180 |
| TACGAACAGC | GCCTGAAAGT | GCTGGAGCGG | GAGGTCCAGC | AGTGTAGCCG | CGTCCTGGG | 240 |
| TGGGTGGCCG | ANGCCTGANC | CGCTCTGCCT | TGCTGCCCG | ANGTGGGCCG | CCACCCCCCTG | 300 |
| ACCTGCCTGG | GTCCAAACAC | TGAGCCCTGC | TGGCCGACTT | CAAGGANAAC | CCCCACANGG | 360 |
| GGATTTGCT | CCTANANTAA | GGCTCATCTG | GGCCTCGGCC | CCCCCACCTG | GTTGGCCTTG | 420 |
| TCTTGANGT | GAGCCCCATG | TCCATCTGGG | CCACTGTCTG | GACCACCTT | NGGGAGTGT | 480 |
| CTCCTTACAA | CCACANNATG | CCCGGCTCT | CCCGGAAACC | ANTCCCANCC | TGNGAAGGAT | 540 |
| CAAGNCCTGN | ATCCACTNN | NCTANAACCG | GCCNCNC | CNGTGGAAC | CNCCTTNTGT | 600 |
| TCCCTTTCNT | TNAGGTTAA | TNNCGCCTTG | GCCTTNCCAN | NGTCCTNCNC | NTTTTCCNNT | 660 |
| GTTNAAATTG | TTANGCNCC | NCCNNTCCCN | CNNCNCCNAN | CCCGACCCNN | ANNTTNNANN | 720 |
| NCCCTGGGGT | NCCNCNGAT | TGACCCNNCC | NCCCTNTANT | TGCNTTNGGG | NNCNNTGCC | 780 |
| CTTCCCTCT | NGGGANNCG | | | | | 799 |

(2) INFORMATION FOR SEQ ID NO:9:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 801 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

| | | | | | | |
|-------------|------------|------------|------------|------------|------------|-----|
| ACGCCTTGAT | CCTCCAGGC | TGGGACTGGT | TCTGGGAGGA | GCCGGGCATG | CTGTGGTTTG | 60 |
| TAANGATGAC | ACTCCCAAAG | GTGGTCTG | CAGTGGCCCA | GATGGACATG | GGGCTCACCT | 120 |
| CAAGGACAAG | GCCACCAGGT | GGGGGGCCG | AAGCCCACAT | GATCCTTACT | CTATGAGCAA | 180 |
| AATCCCCTGT | GGGGGCTCT | CCTTGAAGTC | CGCCANCAGG | GCTCAGTCTT | TGGACCCANG | 240 |
| CAGGTCTATGG | GGTTGTGNC | CAACTGGGG | CCNCAACGCA | AAANGGCNCA | GGGCCTCNGN | 300 |
| CACCCCATCCC | ANGACGCGG | TACACTNCTG | GACCTCCNC | TCCACCACTT | TCATGCGCTG | 360 |
| TTCNTACCCG | CGNATNTGTC | CCANCTGTT | CNGTGCNAC | TCCANCTTCT | NGGACGTGCG | 420 |
| CTACATACCG | CCGGANTCNC | NCTCCCGCTT | TGTCCTATC | CACGTNCCAN | CAACAAATT | 480 |
| CNCCNTANTG | CACCNATTCC | CACNTTNNC | AGNTTCCNC | NNCGNGCTTC | CTTNTAAAAG | 540 |
| GGTTGANCCC | CGGAAAATNC | CCCAAAGGGG | GGGGGCCNGG | TACCCAAC | CCCCCTNATA | 600 |
| GCTGAANTCC | CCATNACCN | GNCTCNATGG | ANCCNTCCNT | TTAANNACN | TTCTNAACTT | 660 |
| GGGAANANCC | CTCGNCCNTN | CCCCNNTAA | TCCCNCCCTG | CNANGNNCN | CCCCNNNTCC | 720 |
| NCCNNNTNG | GCNTNTNANN | CNAAAAAGGC | CCNNANCAA | TCTCCTNNCN | CCTCANTTCG | 780 |
| CCANCCCTCG | AAATCGGCCN | C | | | | 801 |

(2) INFORMATION FOR SEQ ID NO:10:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 789 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

| | | | | | | |
|------------|------------|------------|------------|------------|------------|-----|
| CACTCTATNT | GGCCAGTGTG | GCAGCTTCC | CTGTGGCTGC | CGGTGCCACA | TGCCTGTCCC | 60 |
| ACAGTGTGGC | CGTGGTGACA | GCTTCAGCCG | CCCTCACCGG | GTTCACCTTC | TCAGCCCTGC | 120 |
| AGATCCTGCC | CTACACACTG | GCCTCCCTCT | ACCACCGGGA | GAAGCAGGTG | TTCTGCCCA | 180 |
| AATACCGAGG | GGACACTGGA | GGTGCTAGCA | GTGAGGACAG | CCTGATGACC | AGCTTCTGC | 240 |
| CAGGCCCTAA | GCCTGGAGCT | CCCTTCCCTA | ATGGACACGT | GGGTGCTGGA | GGCAGTGGCC | 300 |
| TGCTCCACC | TCCACCCGCG | CTCTGCGGGG | CCTCTGCCTG | TGATGTCTCC | GTACGTGTTG | 360 |
| TGGTGGGTGA | GCCCACCGAN | GCCAGGGTGG | TTCCGGGCCG | GGGCATCTGC | CTGGACCTCG | 420 |
| CCATCCTGGA | TAGTGCTTCC | TGCTGTCCCA | NGTGGCCCA | TCCCTGTTA | TGGGCTCCAT | 480 |
| TGTCCAGCTC | AGCCAGTCTG | TCACTGCCTA | TATGGTGTCT | GCCGCAGGCC | TGGGCTGGT | 540 |

| | |
|--|-----|
| CCCATTTACT TTGCTACACA GGTANTATT GACAAGAACG ANTTGGCAA AATCTCAGCG | 600 |
| TTAAAAAATT CCAGCAACAT TGGGGGTGGA AGGCCTGCCT CACTGGGTCC AACTCCCCGC | 660 |
| TCCCTTAAAC CCCATGGGSC TGCCGGCTTG GCCGCCAATT TCTGTTGCTG CCAAANTNAT | 720 |
| GTCGGCTCTCT GCTGCCACCT GTTGCTGGCT GAAGTGCNTA CNGCNCANCT NGGGGGGTNG | 780 |
| GGNGTTCCCC | 789 |

(2) INFORMATION FOR SEQ ID NO:11:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 772 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

| | |
|--|-----|
| CCCACCCCTAC CCAAATATTA GACACCAACA CAGAAAAGCT AGCAATGGAT TCCCTTCTAC | 60 |
| TTTGTAAAT AAATAAGTTA AATATTAAA TGCTGTGTC TCTGTGATGG CAACAGAAGG | 120 |
| ACCAACAGGC CACATCCTGA TAAAAGGTA GAGGGGGGTG GATCAGCAAA AAGACAGTGC | 180 |
| TGTGGGCTGA GGGGACCTGG TTCTTGTGTG TTGCCCCCTCA GGACTCTTCC CCTACAAATA | 240 |
| ACTTTCATAT GTTCAAATCC CATGGAGGAG TGTTCATCC TAGAAACTCC CATGCAAGAG | 300 |
| CTACATTTAAA CGAACGCTGCA GGTAAAGGGG CTTANAGATG GGAACACCAGG TGACTGAGTT | 360 |
| TATTCACTC CCAAAAACCC TTCTCTAGGT GTGCTCAAC TAGGAGGCTA GCTGTTAAC | 420 |
| CTGAGCCTGG GTAATCCACCC TGCAAGTCC CGCATTCCA GTGCATGGAA CCCTCTGGC | 480 |
| CTCCCTGTAT AAGTCCAGAC TGAAACCCCC TTGGAAGGNC TCCAGTCAGG CAGCCCTANA | 540 |
| AACTGGGAA AAAAGAAAAG GACGCCCAN CCCCCAGCTG TGCANCTACG CACCTCAACA | 600 |
| GCACAGGGTG GCAGCAAAAA ACCACTTTA CTTTGGCACA AACAAAAACT NGGGGGGCA | 660 |
| ACCCCGGCAC CCCNANGGGG GTTAACAGGA ANCNGGNAA CNTGGAACCC AATTNAGGCA | 720 |
| GGCCCNCCAC CCCNAATNTT GCTGGAAAT TTTCTCCC CTAATTNTT TC | 772 |

(2) INFORMATION FOR SEQ ID NO:12:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 751 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

| | |
|---|-----|
| GCCCCAATTG CAGCTGCCAC ACCACCCACG GTGACTGCAT TAGTTGGAT GTCATACAAA | 60 |
| AGCTGATTGA AGCAACCCCTC TACTTTTG TGCTGAGCT TTTGCTTGGT GCAGGTTCA | 120 |
| TTGGCTGTGT TGGTGACGTT GTCATTGCAA CAGAATGGGG GAAAGGCCT GTTCTCTTG | 180 |
| AAGTANGGTG AGTCCTAAA ATCCGTATAG TTGGTGAAGC CACAGCACTT GAGCCCTTC | 240 |
| ATGGTGGTGT TCCACACTTG AGTGAAGTCT TCCGGGAAC CATAATCTT CTGATGGCA | 300 |
| GGCACTACCA GCAACGTCA GGAAGTCTC AGCCATTGTG GTGTACACCA AGGCGACAC | 360 |
| AGCAGCTGCN ACCTCAGCAA TGAAGATGAN GAGGAGATG AAGAAGAACG TCNCGAGGGC | 420 |
| ACACTTGCTC TCAGTCTTAN CACCATANCA GCCCNTGAAA ACCAANANCA AAGACCACNA | 480 |
| CNCCGGCTGC GATGAAGAAA TNACCCNCG TTGACAAACT TGCATGGCAC TGGGANCCAC | 540 |
| AGTGGCCNA AAAATCTCA AAAAGGATGC CCCATCNATT GACCCCCAA ATGCCCACTG | 600 |
| CCAACAGGGG CTGCCCCACN CNCNNAAAGA TGACCNATT GNACAAAGATC TNCNTGGCT | 660 |
| TNATNAACNT GAACCTGCN TNGTGGCTCC TGTTCAGGNC CNNGGCCTGA CTTCTNAANN | 720 |
| AANGAACTCN GAAGNCCCCA CNGGGANNNC G | 751 |

(2) INFORMATION FOR SEQ ID NO:13:

- (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 729 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

| | | | | | | |
|-------------|------------|-------------|------------|------------|-------------|-----|
| GAGCCAGGGCG | TCCCTCTGCC | TGCCCACCTCA | GTGGCAACAC | CCGGGAGCTG | TTTTGTCC | 60 |
| TGTGGANCT | CAGCAGTNCC | CTCTTCAGA | ACTCANTGCC | AAGANCCCTG | AACAGGAGCC | 120 |
| ACCATGCAGT | GCTTCAGCTT | CATTAAGACC | ATGATGATCC | TCTTCATTTT | GCTCATCTTT | 180 |
| CTGTGTGGT | CAGCCCTGTT | GGCAGTGGC | ATCTGGGTGT | CAATCGATGG | GGCATCCTTT | 240 |
| CTGAAGATCT | TCGGGCCACT | GTCGTCAGT | GCCATGCAGT | TTGTCAACGT | GGGCTACTTC | 300 |
| CTCATCGCAG | CCGGCGTTG | GGTCTTAGCT | CTAGGTTTCC | TGGGCTGCTA | TGGTGCTAAG | 360 |
| ACTGAGAGCA | AGTGTGCCCT | CGTGACGTT | TTCITCATCC | TCCTCCTCAT | CTTCATTGCT | 420 |
| GAGGTTGCAA | TGCTGTGGTC | GCCTTGGTGT | ACACCACAAT | GGCTGAGCAC | TTCCCTGACGT | 480 |
| TGCTGGTAAT | GCCTGCCATC | AANAAAAGAT | TATGGGTTCC | CAGGAANACT | TCACTCAAGT | 540 |
| GTTGGAACAC | CACCATGAAA | GGGCTCAAGT | GCTGTGGCTT | CNNCCAACTA | TACGGATT | 600 |
| GAAGANTCAC | CTACTTCAAA | GAAAANAGTG | CCTTCCCCC | ATTCTGTTG | CAATTGACAA | 660 |
| ACGTCCCCAA | CACAGCCAAT | TGAAAACCTG | CACCCAACCC | AAANGGTCC | CCAACCANAA | 720 |
| ATTNAAGGG | | | | | | 729 |

(2) INFORMATION FOR SEQ ID NO:14:

- (i) SEQUENCE CHARACTERISTICS:

 - (A) LENGTH: 816 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

| | | | | | | |
|-------------|------------|-------------|-------------|------------|------------|-----|
| TGCTCTTCCT | CAAAGTTGTT | CTTGTGCCA | TAACACCAC | CATAGGTAAA | GCGGGCGCAG | 60 |
| TGTTCGCTGA | AGGGGTTGTA | GTACCAAGCGC | GGGATGCTCT | CCTTGCAGAG | TCCTGTGCT | 120 |
| GGCAGGTCCA | CGCAGTGCC | TTTGTCACTG | GGGAAATGGA | TGCGCTGGAG | CTCGTCAAAG | 180 |
| CCACTCGTGT | ATTTTCACA | GGCAGCCTCG | TCCGACGCGT | CGGGGCAGTT | GGGGGTGCT | 240 |
| TCACACTCCA | GGAAACTGTC | NATGCAGCAG | CCATTGCTGC | AGCGGAACTG | GGTGGGCTGA | 300 |
| CANGTGCCAG | AGCACACTGG | ATGGCGCTT | TCCATGNNA | GGGCCCTGNG | GGAAAGTCCC | 360 |
| TGANCCCAN | ANCTGCCCT | CAAANGCCC | ACCTTGACACA | CCCCGACAGG | CTAGAATGGA | 420 |
| ATCTTCTTCC | CGAAAGGTAG | TTNTTCTTGT | TGCCCAANCC | ANCCCCNTAA | ACAAACTCTT | 480 |
| GCAANATCTGC | TCCGNNGGGG | TCTNTTACCC | ANCCTGGAA | AAGAACCCCA | GGCNGCGAAC | 540 |
| CAANCTTGT | TGGATNCGAA | GCNATAATCT | NTCTNTCTGC | TTGGTGGACA | GCACCANTNA | 600 |
| CTGTNNANCT | TTAGNCCNTG | GTCCTCNTGG | GTTGNNCTTG | AACTTAATCN | CCNNTCAACT | 660 |
| GGGACAAGGT | AANTNGCCNT | CCTTNAATT | CCCNANCNTN | CCCCCTGGTT | TGGGGTTT | 720 |
| CNCNCTCCTA | CCCCAGAAAN | NCCGTGTTCC | CCCCCAACTA | GGGGCCNAAA | CCNNTNTTC | 780 |
| CACAACCCTN | CCCCACCCAC | GGGTTNGNT | GGTTNG | | | 816 |

(2) INFORMATION FOR SEQ ID NO:15:

- (i) SEQUENCE CHARACTERISTICS:

 - (A) LENGTH: 783 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

| | | | | | | |
|------------|-------------|-------------|------------|-------------|-------------|-----|
| CCAAGGCCTG | GGCAGGCATA | NACTTGAAGG | TACAACCCCA | GGAAACCCCTG | GTGCTGAAGG | 60 |
| ATGTGGAAA | CACAGATTGG | CGCCTACTGC | GGGGTGACAC | GGATGTCAGG | GTAGAGAGGA | 120 |
| AAGACCCAAA | CCAGGGTGGAA | CTGTGGGGAC | TCAAGGAANG | CACCTACCTG | TTCCAGCTGA | 180 |
| CAGTGAATG | CTCAGACCAC | CCAGAGGACA | CGGCCAACGT | CACAGTCACT | GTGCTGTCCA | 240 |
| CCAAGCAGAC | AGAAGACTAC | TGCCTCGCAT | CCAACAANGT | GGGTGCGCTGC | CGGGGCTCTT | 300 |
| TCCCACGCTG | GTACTATGAC | CCCACGGAGC | AGATCTGCAA | GAGTTTCGTT | TATGGAGGCT | 360 |
| GCTTGGGCAA | CAAGAACAAAC | TACCTTCGGG | AAGAAGAGTG | CATTCTANCC | TGTCNGGGTG | 420 |
| TGCAAGGTGG | GCCTTTGANA | NGCANCTCTG | GGGCTCANGC | GACTTTCCCC | CAGGGCCCCCT | 480 |
| CCATGGAAAG | GCGCCATCCA | NTGTTCTCTG | GCACCTGTCA | GCCCACCCAG | TTCCGCTGCA | 540 |
| NCAATGGCTG | CTGCATCNAC | ANTTCTCTNG | AATTGTGACA | ACACCCCCCA | NTGCCCCCAA | 600 |
| CCCTCCCAAC | AAAGCTTCCC | TGTTAAAAAA | TACNCCANTT | GGCTTTTNAC | AAACNCCCCG | 660 |
| CNCCTCCNTT | TTCCCNNTN | AAACAAAGGGC | NCTNGCNTTT | GAACGTGCCN | AAACCNNGAA | 720 |
| TCTNCCNNNG | AAAAANTNCC | CCCCCTGGTT | CCTNNAANCC | CCTCCNCNAA | ANCTNCCCC | 780 |
| CCC | | | | | | 783 |

(2) INFORMATION FOR SEQ ID NO:16:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 801 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

| | | | | | | |
|-------------|------------|------------|------------|------------|------------|-----|
| GCCCCAATTG | CAGCTGCCAC | ACCACCCACG | GTGACTGCAT | TAGTTGGAT | GTCATACAAA | 60 |
| AGCTGATTGA | AGCAACCTCT | TACTTTTG | TCGTGAGCCT | TTTGCTTGGT | GCAGGTTTCA | 120 |
| TTGGCTGTGT | TGGTGACGTT | GTCATTGCAA | CAGAATGGGG | GAAAGGCAC | GTTCTCTTG | 180 |
| AAGTAGGGTG | AGTCCCTCAA | ATCCGTATAG | TTGGTGAAGC | CACAGCACTT | GAGCCCTTC | 240 |
| ATGGTGGTGT | TCCACACTTG | AGTGAAGTCT | TCCCTGGAAC | CATAATCTTT | CTTGATGGCA | 300 |
| GGCACTACCA | GCAACGTCAG | GAAGTGTCA | GCCATTGTGG | TGTACACCAA | GGCGACCCAA | 360 |
| GCAGCTGCAA | CCTCAGCAAT | GAAGATGAGG | AGGAGGATGA | AGAAGAACGT | CNCGAGGGCA | 420 |
| CACTTGCTCT | CCGTCTTAGC | ACCATAGCAG | CCCANGAAAC | CAAGAGCAAA | GACCACAA | 480 |
| CCNGCTGCGA | ATGAAAGAAA | NTACCCACGT | TGACAAACTG | CATGGCCACT | GGACGACAGT | 540 |
| TGGCCCGAAN | ATCTTCAGAA | AAGGGATGCC | CCATCGATTG | AACACCCANA | TGCCCACTGC | 600 |
| CNACAGGGCT | GCNCNCNCN | GAAAGAATGA | GCCATTGAAG | AAGGATCNTC | NTGGTCTTAA | 660 |
| TGAACGTGAAA | CCTTGCATGG | TGGCCCTGT | TCAGGGCTCT | TGGCAGTGAA | TTCTGANAAA | 720 |
| AAGGAACNGC | NTNAGCCCCC | CCAAANGANA | AAACACCCCA | GGGTGTTGCC | CTGAATTGGC | 780 |
| GGCCAAGGAN | CCCTGCCCN | G | | | | 801 |

(2) INFORMATION FOR SEQ ID NO:17:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 740 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

| | | | | | | |
|------------|------------|------------|------------|------------|------------|-----|
| GTGAGAGCCA | GGCGTCCCTC | TGCCTGCCCA | CTCAGTGGCA | ACACCCGGGA | GCTGTTTGT | 60 |
| CCTTGTGGA | GCCTCAGCAG | TTCCCTCTT | CAGAACTCAC | TGCCAAGAC | CCTGAACAGG | 120 |
| AGCCACCATG | CAGTCTTCA | GCTTCATTAA | GACCATGATG | ATCCCTTCA | ATTGCTCAT | 180 |
| CTTTCTGTGT | GGTGCAGCCC | TGTTGGCAGT | GGGCATCTGG | GTGTCAATCG | ATGGGGCATC | 240 |
| CTTTCTGAAG | ATCTTCGGGC | CACTGTGTC | CAGTGCATG | CAGTTGTCA | ACGTGGGCTA | 300 |
| CTTCCTCATC | GCAGCCGGCG | TTGTGGCTT | TGCTCTGGT | TCCCTGGGCT | GCTATGGTGC | 360 |

| | |
|---|-----|
| TAAGACGGAG AGCAAGTGTG CCCTCGTGAC GTTCTTCTTC ATCCTCCTCC TCATCTTCAT | 420 |
| TGCTGAAGTT GCAGCTGCTG TGGTCGCCCT GGTGTACACC ACAATGGCTG AACCATTCT | 480 |
| GACGTTGCTG GTANTGCCCT CCATCAANAA AGATTATGGG TTCCCAGGAA AAATTCACTC | 540 |
| AANTNTGAA CACCNCCATG AAAAGGGCTC CAATTCTGN TGCGCTTCCCC AACTATAACG | 600 |
| GAATTTGAA AGANTCNCCC TACTTCAA AAAAANANT TGCGCTTNCC CCCNTCTGT | 660 |
| TGCAATGAAA ACNTCCAAN ACNGCCAATN AAAACCTGCC CNNNCAAAAA GGNTCNAAA | 720 |
| CAAAAAAANT NNAAGGGTTN | 740 |

(2) INFORMATION FOR SEQ ID NO:18:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 802 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

| | |
|--|-----|
| CCGCTGGTTG CGCTGGTCCA GNGNAGGCCAC GAAGCACGTC AGCATACACA GCCTCAATCA | 60 |
| CAAGGTCTTC CAGCTGCCGC ACATTACGCA GGGCAAGAGC CTCCAGCAAC ACTGCATATG | 120 |
| GGATACACTT TACTTTAGCA GCCAGGGTGA CAACTGAGAG GTGCGAAGC TTATTCTTCT | 180 |
| GAGCCCTGTG TAGTGGAGGA AGATCCGGG CTTCAGCTAA GTAGTCAGCG TATGTCCCAT | 240 |
| AAGCAAACAC TGTGAGCAGC CGGAAGGTAG AGGCAAAGTC ACTCTCAGCC AGCTCTCTAA | 300 |
| CATTGGGCAT GTCCAGCACT TCTCCAAACA CGTAGACACC AGNGGCCTCC AGCACCTGAT | 360 |
| GGATGAGTGT GGCCAGCGCT GCCCCCTTGG CCGACTTGGC TAGGAGCAGA AATTGCTCCT | 420 |
| GGTTCTGCCCT TGTCACCTTC ACTTCCGCAC TCATCACTGC ACTGAGTGTG GGGGACTTGG | 480 |
| GCTCAGGATG TCCAGAGACG TGGTCCGCC CCCTCNCTTA ATGACACCGN CCANNCAACC | 540 |
| GTCGGCTCCC GCCGANTGNG TTCGTCGTNC CTGGTCAGG GTCTGCTGGC CNCTACTTGC | 600 |
| AANCTTCGTC NGGCCCATGG AATTCAACCNC ACCGGAACTN GTANGATCCA CTNNTTCTAT | 660 |
| AACCGGNNGC CACCGCNNTT GGAACCTCCAC TCTTNTTNCC TTACTTGTAG GGTAAAGGTC | 720 |
| ACCCITNNCG TTACCTTGTG CCAAACCNNT CCNTGTGTG ANALNGTNAA TCNGGNCCNA | 760 |
| TNCCANCCNC ATANGAAGCC NG | 802 |

(2) INFORMATION FOR SEQ ID NO:19:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 731 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

| | |
|---|-----|
| CNAAGCTTCC AGGTNACGGG CGCGNAANCC TGACCCNAGG TANCANAANG CAGNCNGCGG | 60 |
| GAGCCCACCG TCACGNNGNG GNGTCTTTAT NGGAGGGGGC GGAGCCACAT CNCTGGACNT | 120 |
| CNTGACCCCCA ACTCCCCNCC NCNCANTGCA GTGATGAGTG CAGAACTGAA GGTNACGTGG | 180 |
| CAGGAACCAA GANCAAANN NC TGCTCCNNTC CAAGTCGGCN NAGGGGGCGG GGCTGGCCAC | 240 |
| GCNCATCCNT CNAGTGTCTN AAAGCCCCNN CCTGTCTACT TGTGGAGA ACNGCENNNGA | 300 |
| CATGCCCAAGN GTTANATAAAC NGGCNGAGAG TNANTTGCC TCTCCCTTCC GGCTGCGCAN | 360 |
| CGNGTNTGCT TAGNGGACAT AACCTGACTA CTTAACTGAA CCCNNGAATC TNCCNCCCT | 420 |
| CCACTAAGCT CAGAACAAA AACTTCGACA CCACCTCANTT GTCACCTGNC TGCTCAAGTA | 480 |
| AAAGTGTACCC CATNCCCAAT GTNTGCTNGA NGCTCTGNCC TGCNTTANTG TCGGTCTGG | 540 |
| GAAGACCTAT CAATTNAAGC TATGTTCTG ACTGCCTT GCTCCCTGNA ACAANCNACC | 600 |
| CNNCNNTCCA AGGGGGGGNC GGCCCCAAT CCCCCAAC NTNAATTNAN TTTANCCCN | 660 |
| CCCCNNGGCC CGGCCTTTA CNANCNTCNN NNACNGGNA AAACCNNGC TTNCCCAAC | 720 |
| NNAATCCNCC T | 731 |

(2) INFORMATION FOR SEQ ID NO:20:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 754 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

| | | | |
|----------------------|----------------------|------------------------|-----|
| TTTTTTTTT TTTTTTTTTT | AAAAACCCC CTCCATTNAA | TGAAACTTC CGAAATTGTC | 60 |
| CAACCCCCCTC | NTCCAAATNN CCNTTCCGG | GNGGGGGTTC CAAACCCAAN | 120 |
| ANNTTAAATT | AAATNTTNTT | TGGNGGNNA ANCCNAATGT | 180 |
| TNANCTTNA | TNCCCTGGAAA | CCNGTNGNTT CCAAAAATNT | 240 |
| AAATNGTTNA | NGGAAAACCC | TTAACCCCTTA ANTCCCTCCG | 300 |
| NNCCAATTGT | TTTNGCCAC | AAGGGTGTGTT GAAGGNTNAA | 360 |
| GGNNANCCCG | GGTTANTNAA | TCCCCCNNA CCCAATTATA | 420 |
| GANCCCNCGG | GAATTAACGG | CCGGANTTTT TTNGAATTGG | 480 |
| GGTTNGGGNC | AGGNCCNAAT | TNTTGGGGGG CNGGNNCCCG | 540 |
| CCAGGNTGAG | NNTNGGGTTT | CCCTCCNAGA AAAAAANCTC | 600 |
| GGGGCCTGGG | ATTTNTTTC | CANGGCCCCCT CTCGNANAGT | 660 |
| TTTGNTCNCC | GGCCCCNCCN | TCCCCCCCCC CCNGGGANAG | 720 |
| AGTCCNTTGN | AGGGNTAAAN | AGGTTNGNGT | 754 |

(2) INFORMATION FOR SEQ ID NO:21:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 755 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

| | | |
|--|-----------------------|-----|
| ATCANCCCAT GACCCNAAC NNNGGACCNC TCANCCGGNC | NNNCNACCNC CGGCCNATCA | 60 |
| NNGTNAGNNC ACTNCNNTT NATCACNCCC | CNCCNACTAC GCCNCNANC | 120 |
| NNCANATNCC ACTGANNGCG | CGANGTNGAN NGAGAAANCT | 180 |
| CCAGCTGTCC NANAANGCCT | NNNATACNGG NNNATCCAAT | 240 |
| NNCNCNANAT GATTTCTN | ANCCGATTAC CCNTNCCCC | 300 |
| CGAAGGCNCT GGNCCNAAGG | NNCGCNCC CCGCTAGNTC | 360 |
| AACTCANCCN | TTCNTGAGTA TCACTCCCCG | 420 |
| AAAAANATCN GATACAAAT | AATTCACCC TACTCAACTC | 480 |
| TTAGNGGTCC NTNAANCNTC | TGNTTATNAC ACTNTGACTG | 540 |
| CTTTCNGACA GCATNTTTG | GAGTCTNCCT TCNCCAATT | 600 |
| GGGCTCNTCT | GGGTCTTTAN NGAATTGCC | 660 |
| AAATTCTNCC | TTACCTTGGG TTCNNCCGGC | 720 |
| AAAAGGTTGT | CAGTTATTAT TTCCNTTTT | 755 |
| TTTGANAAAA | CTTGAAAACG GCCCCCTGGT | |

(2) INFORMATION FOR SEQ ID NO:22:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 849 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

| | | | | | | |
|------------|------------|-------------|--------------|------------|------------|-----|
| TTTTTTTTT | TTTTTANGTG | TNGTCGTGCA | GGTAGAGGCT | TACTACAANT | GTGAANACGT | 60 |
| ACGCTNGGAN | TAANGCGACC | CGANTTCTAG | GANNCCCT | AAAATCANAC | TGTGAAGATN | 120 |
| ATCCCTGNNA | CGGAANGGTC | ACCGGNNNGAT | NNTGCTAGGG | TGNCCNCTCC | CANNNCNTTN | 180 |
| CATAACTCNG | NGGCCCTGCC | CACCACTTC | GGCGGCCNG | NGNCCGGCC | CGGGTCATTN | 240 |
| GNNTTAACCN | CACTNNGCNA | NCGGTTCCN | NCCCNCCNG | ACCCNGGCGA | TCCGGGGTNC | 300 |
| TCTGCTTCC | CCTGNAGNCN | ANAAAANTGGG | CCNCGGNCCC | CTTACCCCT | NNACAAGCCA | 360 |
| CNGCCNTCTA | NCCCNCGCC | CCCCCTCCANT | NNGGGGACT | CCGNANNGCT | CCGTTNCTNG | 420 |
| NNACCCNNN | GGGTNCTCG | GTTGTCGANT | CNACCGNANG | CCANGGATC | CNAAGGAAGG | 480 |
| TGCGTTNTTG | GCCCCTACCC | TTCGCTNCGG | NNCACCCCTTC | CCGACNANGA | NCCGCTCCG | 540 |
| CNCNCGNNG | CCTCNCTCG | CAACACCCCG | NCTCNTCNGT | NCGGNNNNCC | CCCCACCCGC | 600 |
| NCCCTNCNC | NGNCGNANCN | CTCCNCCNCC | GTCTCANNCA | CCACCCCGCC | CCGCCAGGCC | 660 |
| NTCANCCACN | GGNNGACNNG | NAGCNCNNTC | GCNC CGC GCG | GCNCNCNCCT | CGCCNCNGAA | 720 |
| CTNCNTCNGG | CCANTNNCGC | TGAANCCNA | CNAACGCGG | CTGCGCGGCC | CGNAGCGNCC | 780 |
| NCCTCCNGA | GTCCTCCCGN | CTTCCNACCC | ANGNNTTCCN | CGAGGACACN | NNACCCCGCC | 840 |
| NNCANGCGG | | | | | | 849 |

(2) INFORMATION FOR SEQ ID NO:23:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 872 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

| | | | | | | |
|------------|-------------|-------------|------------|-------------|-------------|-----|
| GCGCAAACTA | TACTTCGCTC | GNACTCGTGC | GCCTCGCTNC | TCTTTTCCTC | CGCAACCATG | 60 |
| TCTGACNANC | CCGATTNGGC | NGATATCNAN | AAGNTCGANC | AGTCAAACACT | GANTAACACA | 120 |
| CACACNCNAN | AGANAATCC | NCTGCCCTCC | ANAGTANACN | ATTGAACNNG | AGAACCAANGC | 180 |
| NGGCGAATCG | TAATNAGGGCG | TGCGCCGCCA | ATNTGTCNCC | GTTTATTNTN | CCAGCNTCNC | 240 |
| CTNCCNACCC | TACNTCTTCN | NAGCTGTCCN | ACCCCTNGTN | CGNACCCCC | NAGGTCGGGA | 300 |
| TCGGGTTNN | NNTGACCGNG | CNNCCCTCC | CCCCNTCCAT | NACGANCCNC | CCGCACCACC | 360 |
| NANNGCNCG | NCCCCGNCT | CTTCGCCNCC | CTGTCCTNN | CCCCGTNGC | CTGGCNCNGN | 420 |
| ACCGCATTGA | CCCTCGCCNN | CTNCNNGAAA | NCGNANACGT | CCGGGTTGNN | ANNANCCTG | 480 |
| TGGGNNNGCG | TCTGCNCCGC | GTTCCTTCCN | NCNNCTTCGA | CCATCTTCNT | TACNGGGTCT | 540 |
| CCNCGCCNTC | TCNNNCACNC | CCTGGGACGC | TNTCCTNTGC | CCCCCTTNAC | TCCCCCCCTT | 600 |
| CGNCGTGNCC | CGNCCCCAC | NTCATTTNCA | NACNTCTTC | ACAANNNCCT | GGNTNNCTCC | 660 |
| CNANCNGNCN | GTCANCCNAG | GGAAAGGGNGG | GGNCCNNNTG | NTTGACGTG | NGGNGANGTC | 720 |
| CGAANANTCC | TCNCNTCNC | CNCTACCCCT | CGGGCGNNCT | CTCNGTTNCC | AACTTANCAA | 780 |
| NTCTCCCCCG | NGNGCNCNTC | TCAGCCTCNC | CCNCCCNCT | CTCTGCANTG | TNCTCTGCTC | 840 |
| TNACCNNTAC | GANTNTTCGN | CNCCCTCTTT | CC | | | 872 |

(2) INFORMATION FOR SEQ ID NO:24:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 815 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

| | | | | | | |
|------------|------------|------------|------------|------------|------------|-----|
| GCATGCAAGC | TTGAGTATTC | TATAGNGTCA | CCTAAATANC | TTGGCNTAAT | CATGGTCNTA | 60 |
| NCTGNCTTCC | TGTGTCAAAT | GTATACNAAN | TANATATGAA | TCTNATNTGA | CAAGANNGTA | 120 |

| | | | | | | |
|-------------|------------|------------|-------------|-------------|------------|-----|
| TCNTNCATTA | GTAACAANTG | TNNTGTCCAT | CCTGTCNGAN | CANATTCCCA | TNNATTNCGN | 180 |
| CGCATTNCN | GCNCANTATN | TAATNGGAA | NTCNNTNNN | NCACCCNAT | CTATCNTNCC | 240 |
| GCNCCCTGAC | TGGNAGAGAT | GGATNANTTC | TNNNTNTGACC | NACATGTTCA | TCTTGGATTN | 300 |
| AANANCCCCC | CGCNGNCCAC | CGGTTNGNNG | CNAGCCNNTC | CCAAGACCTC | CTGTGGAGGT | 360 |
| AACCTGCGTC | AGANNCATCA | AACNTGGAA | ACCCGCNNCC | ANGTNNAAGT | NGNNNCANAN | 420 |
| GATCCCGTCC | AGGNTTNACC | ATCCCTTCNC | AGCGCCCCCT | TTNGTGCCTT | ANAGNGNAGC | 480 |
| GTGTCCNANC | CNCTCAACAT | GANACGCGCC | AGNCCANCCG | CAATTNGGCA | CAATGTCGNC | 540 |
| GAACCCCCCTA | GGGGGANTNA | TNCAAANCCC | CAGGATTGTC | CN CNCANGAA | ATCCCNANC | 600 |
| CCCNCCCTAC | CCNNCTTGGG | GACNGTGACC | AANTCCCGGA | GTNCCAGTCC | GGCCNGNCTC | 660 |
| CCCCACCGGT | NNCCNTGGGG | GGGTGAACNT | CNGNNTCANC | CNGNCGAGGN | NTCGNAAGGA | 720 |
| ACCGGNCCTN | GGNGGAANNG | ANCNNTCNGA | AGNGCCNCNT | CGTATAACCC | CCCCTCNCCA | 780 |
| NCCNACNGNT | AGNTCCCCCC | CNGGGTNCGG | AANGG | | | 815 |

(2) INFORMATION FOR SEQ ID NO:25:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 775 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

| | | | | | | |
|------------|------------|------------|------------|-------------|------------|-----|
| CCGAGATGTC | TCGCTCCGTG | GCCTTAGCTG | TGCTCGCGCT | ACTCTCTCTT | TCTGGCCTGG | 60 |
| AGGCTATCCA | GCGTACTCCA | AAGATTCAAG | TTTACTCACG | TCATCCAGCA | GAGAATGGAA | 120 |
| AGTCAAATT | CCTGAATTGC | TATGTGTCTG | GGTTCATCC | ATCCGACATT | GAANTTGACT | 180 |
| TACTGAAGAA | TGGANAGAGA | ATTGAAAAAG | TGGAGCATTC | AGACTTGTCT | TTCAGCAAGG | 240 |
| ACTGGTCTT | CTATCTCNTG | TACTACACTG | AATTCAACCC | CACTGAAAAAA | GATGAGTATG | 300 |
| CTGCGGTGT | GAACCATGTG | ACTTTGTAC | AGCCAAGAT | AGTTAAGTGG | GATCGAGACA | 360 |
| TGTAAGCAGN | CNNCATGGAA | GTTTGAAGAT | GCCGCATTG | GATTGGATGA | ATTCCAATT | 420 |
| CTGCTTGCTT | GCNTTTAAAT | ANTGATATGC | NTATACACCC | TACCCCTTAT | GNCCCCAAAT | 480 |
| TGTAGGGTTT | ACATNANTGT | TNCNTNGGA | CATGATCTTC | CTTTATAANT | CCNCNTTCG | 540 |
| AATTGCCGT | CNCCCNNGT | NGAATGTTTC | CNNAACCACG | GTGAGCTCCC | CCAGGTCNCC | 600 |
| TCTTACGGAA | GGGCCTGGGC | CNCTTNCAA | GGTTGGGGGA | ACCNAAAATT | TCNCTNTGC | 660 |
| CCNCCCNCCA | CNNTCTTNG | NNNCANTTT | GGAACCCCTC | CNATTCCCT | TGGCCTCNNA | 720 |
| NCCTNNCTA | ANAAAACTTN | AAANGTNGC | NAAAANNTTN | ACTTCCCCCC | TTACC | 775 |

(2) INFORMATION FOR SEQ ID NO:26:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 820 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

| | | | | | | |
|-------------|------------|------------|-------------|-------------|------------|-----|
| ANATTANTAC | AGTGTAATCT | TTTCCCAGAG | GTGTGTANAG | GGAACGGGGC | CTAGAGGCAT | 60 |
| CCCANAGATA | NCTTATANCA | ACAGTGTTT | GACCAAGAGC | TGCTGGCAC | ATTTCTGCA | 120 |
| GAAAAGGTGG | CGGTCCCCAT | CACTCCCT | CTCCCATAGC | CATCCCAGAG | GGGTGAGTAG | 180 |
| CCATCANGCC | TCGGTGGGA | GGGAGTCANG | GAAACAAACAN | ACACAGAGC | ANACAGACCA | 240 |
| NTGATGACCA | TGGGCGGGAG | CGAGCCTCTT | CCCTGNACCG | GGGTGGCANA | NGANAGCCTA | 300 |
| NCTGAGGGT | CACACTATAA | ACGTTAACGA | CCNAGATNAN | CACCTGCTTC | AAGTGCACCC | 360 |
| TTCCCTACCTG | ACNACCAGNG | ACCNNAACT | GCNGCCTGGG | GACAGCNCCTG | GGANCAGCTA | 420 |
| ACNNAGCACT | CACCTGCCCC | CCCATGGCCG | TNCGNTCCC | TGGTCTTGNC | AAGGGAAGCT | 480 |
| CCCTGTTGGA | ATTNCGGGG | NACCAAGGG | NCCCCCTCCT | CCANCTGTGA | AGGAAAANN | 540 |
| GATGGAATT | TNCCCTTCCG | GCCNNTCCCC | TCTTCTTTA | CACGCCCT | NNTACTCN | 600 |

| | |
|--|-----|
| TCCCTCTNTT NTCCTGNCNC ACTTTNACC CCNNNATTTC CCTTNATTGA TCGGANNCTN | 660 |
| GANATTCCAC TNNCGCCTNC CNTCNATCNG NAANACNAAA NACTNTCTNA CCCNGGGAT | 720 |
| GGNNNCCTCG NTCATCCTCT CTNTTCNCT ACCNCCNNTT CTTTGCCCTC CCTTNGATCA | 780 |
| TCCAACCNTC GNTGCCNTN CCCCCCNNTN TCCTTNCCC | 820 |

(2) INFORMATION FOR SEQ ID NO:27:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 818 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

| | |
|--|-----|
| TCTGGGTGAT GGCCTCTTCC TCCTCAGGGA CCTCTGACTG CTCTGGGCCA AAGAATCTCT | 60 |
| TGTTTCTTCT CCGAGCCCCA GGCAGGGGTG ATTCAAGCCCT GCCCAACCTG ATTCTGATGA | 120 |
| CTGCGGATGC TGTGACGGAC CCAAGGGCA AATAGGGTCC CAGGGTCCAG GGAGGGGGCGC | 180 |
| CTGCTGAGCA CTTCCGCCCC TCACCCCTGCC CAGCCCTGCC CATGAGCTCT GGGCTGGGTC | 240 |
| TCCGCTCTCCA GGGTTCTGCT CTTCCANGCA NGCCANCAAG TGGCGCTGSS CCACACTGGC | 300 |
| TTCTTCTCTGC CCCNTCCCTG GCTCTGANTC TCTGCTTCC TGTCTGTGC ANGCNCCTTG | 360 |
| GATCTCAGTT TCCCTCNCTC ANNAACTCT GTTCTGANN TCTTCANTTA ACTNTGANTT | 420 |
| TATNACCNAN TGGNCTGTC TGTCNNATT TAATGGCCN GACCGGCTAA TCCCTCCCTC | 480 |
| NCTCCCTTCC ANTTCNMNA ACCNGCTTNC CNTCNCCTCC CCNTANCCCG CCNGGGAANC | 540 |
| CTCCCTTGCC CTNACCANGG GCCNNNACCG CCCNTNNCTN GGGGGGCNNG GTNNCTNCNC | 600 |
| CTGNTNNCCC CNCTCNNTN TNCCCTGTC CNNCNCGCN NNGCANNNTTC NCNGTCCNN | 660 |
| TNNCTCTTCN NGTNTCGNAA NGNTNCNTN TNNNNNGNCN NGNTNNNTNCN TCCCTCTCNC | 720 |
| CNNNTGNANG TNNTTNNNNC NCNGNNCCC NNNCNNNNN NGNNNTNNN TCTNCNCNGC | 780 |
| CCNNCCCCC NGNATTAAGG CCTCCNNCTC CGGCCNC | 818 |

(2) INFORMATION FOR SEQ ID NO:28:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 731 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

| | |
|--|-----|
| AGGAAGGGCG GAGGGATATT GTANGGGATT GAGGGATAGG AGNATAANGG GGGAGGTGTG | 60 |
| TCCCAACATG ANGGTGNNGT TCTCTTTGA ANGAGGGTTG NGTTTTTANN CCNGGTGGGT | 120 |
| GATTNAACCC CATTGTATGG AGNNAAGGN TTNAGGGAT TTTTCGGCTC TTATCAGTAT | 180 |
| NTANATTCCCT GTNAATCGGA AAATNATNTT TCNNCNGGAA ATNTTGCTC CCATCCGNA | 240 |
| ATTNCTCCCG GGTAGTGCAT NTTNGGGGN CNGCCANGTT TCCCAGGCTG CTANAATCGT | 300 |
| ACTAAAGNTT NAAGTGGGAN TNCAAATGAA AACCTNNCAC AGAGNATCCN TACCCGACTG | 360 |
| TNNNTTNCCCT CGCCCTNTG ACTCTGCNNG AGCCAATAC CCNNGNAT GTCNCCNGN | 420 |
| NNNGCGNCNC TGAAANNNC TCGNGGCTNN GANCATCANG GGGTTTCGCA TCAAAAGCNN | 480 |
| CGTTTCNCAT NAAGGCACCT TNGCCTCATC CAACCNCTNG CCCTCNNTCA TTTNGCCGTC | 540 |
| NGGTTCNCCCT ACGCTNNNTG CNCCTNNNTN GANATTTNC CCGCCTNGGG NAANCCTCCT | 600 |
| GNAATGGGTA GGGNCTTNTC TTTTNACCNN GNGGTNTACT AATCNNTCTNC ACGCNTNCTT | 660 |
| TCTCNACCCC CCCCCCTTTT CAATCCANC GGCNAATGGG GTCTCCCNNT CGANGGGGG | 720 |
| NNNCCCANNC C | 731 |

(2) INFORMATION FOR SEQ ID NO:29:

- (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 822 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

| | | | | | | |
|-------------|-------------|------------|-------------|-------------|--------------|-----|
| ACTAGTCCAG | TGTGGTGGAA | TTCCATTGTG | TTGGGGNCNC | TTCTATGANT | ANTNTTAGAT | 60 |
| CGCTCANACC | TCACANCCCTC | CCNACNANGC | CTATAANGAA | NANNAATAGA | NCTGTNCNN | 120 |
| ATNTNTACNC | TCATANNCCT | CNNNACCAC | TCCCTCTTAA | CCCNCTACTGT | GCCTATNGCN | 180 |
| TNNCTANTCT | NTGCCGCCTN | CNANCCACCN | GTCGGGCNAC | CNCNNGNATT | CTCNATCTCC | 240 |
| TCNCCATNTN | GCCTANANTA | NGTNCATACC | CTATAACCTAC | NCCAATGCTA | NNNCTAACNC | 300 |
| TCCATNANTT | ANNNTAACTA | CCACTGACNT | NGACTTTNCNC | ATNANCTCCT | AATTGAAATC | 360 |
| TACTCTGACT | CCCCACNGCCT | ANNNATTAGC | ANCNTCCCCC | NACNATNTCT | CAACCAAATC | 420 |
| NTCAACAAACC | TATCTANCTG | TTCNCCAACC | NTTNCCCTCG | ATCCCCNNAC | AACCCCCCTC | 480 |
| CCAAAATACCC | NCCACCTGAC | NCCTAACCCN | CACCATCCCG | GCAAGCCNAN | GGNCATTAN | 540 |
| CCACTGGAAT | CACNATNGGA | AAAAAAAC | CCNAACTCTC | TANCNCCNAT | CTCCCCTAACNA | 600 |
| AATNCTCTN | NAATTACTN | NCANTNNCAT | CAANCCACN | TGAAACNNAA | CCCCCTGTTT | 660 |
| TANATCCCTT | CTTTGAAAAA | CCNACCCCTT | ANNNCCCAAC | CTTNGGGCC | CCCCCNCTNC | 720 |
| CCNAATGAAG | GNCNCCCAAT | CNANGAAACG | NCCNTGAAAA | ANCNAGGCNA | ANANNNTCCG | 780 |
| CANATCCTAT | CCCTTANTTN | GGGGNCCCTT | NCCCNNGGCC | CC | | 822 |

(2) INFORMATION FOR SEQ ID NO:30:

- (i) SEQUENCE CHARACTERISTICS:

 - (A) LENGTH: 787 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

| | | | | | | |
|------------|------------|------------|------------|-------------|------------|-----|
| CGGCCGCTG | CTCTGGCACA | TGCCTCCTGA | ATGGCATCAA | AAAGTGATGGA | CTGCCATTG | 60 |
| CTAGAGAAGA | CCTTCTCTCC | TACTGTCATT | ATGGAGCCCT | GCAGACTGAG | GGCTCCCTT | 120 |
| GTCAGGAGGA | TTTGATGTCT | GAAGTCGTGG | AGTGTGGCTT | GGAGCTCCTC | ATCTACATNA | 180 |
| GCTGGAAGCC | CTGGAGGGCC | TCTCTGCCA | GCCTCCCCCT | TCTCTCCACG | CTCTCCANGG | 240 |
| ACACCAGGGG | CTCCAGGCAG | CCCATTATTC | CCAGNANGAC | ATGGTGTTTC | TCCACGCGGA | 300 |
| CCCATGGGGC | CTGNAAGGCC | AGGGTCTCCT | TTGACACCAT | CTCTCCCGTC | CTGCCTGGCA | 360 |
| GGCCGTGGGA | TCCACTANTT | CTANAACGGN | CGCCACCNCG | GTCGGGAGCTC | CAGCTTTTGT | 420 |
| TCCCNNTAAT | GAAGGTTAAT | TGCNCGCTTG | GCGTAATCAT | NGGTCAAAC | TNTTCCTGT | 480 |
| GTAAATTGT | TTNTCCCTC | NCNATTCCNC | NCACATACN | AAACCGGAAN | CATAAAGTGT | 540 |
| TAAAGCCTGG | GGGTNGCCTN | NNGAATNAAC | TNAACTCAAT | TAATTGCGTT | GGCTCATGGC | 600 |
| CCGCTTTCCN | TTCNGGAAAA | CTGTCNTCCC | CTGCTTNTNT | GAATCGGCCA | CCCCCCNGGG | 660 |
| AAAAGCGGTT | TGCNTTTTNG | GGGGNTCCCT | CCNCTTCCCC | CCTCNCTAAN | CCCTNCGCCT | 720 |
| CGGTGTTNC | NGGTNGCGGG | GAANGGGNAT | NNNCTCCNC | NAAGGGGGNG | AGNNNGNTAT | 780 |
| CCCCAAA | | | | | | 787 |

(2) INFORMATION FOR SEQ ID NO:31:

- (i) SEQUENCE CHARACTERISTICS:

 - (A) LENGTH: 799 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

| | | | | | | |
|-------------|------------|------------|------------|------------|------------|-----|
| TTTTTTTTT | TTTTTTGGC | GATGCTACTG | TTTAATTGCA | GGAGGGGGGG | GTGTGTGTAC | 60 |
| CATGTACAG | GGCTATTAGA | AGCAAGAAGG | AAGGAGGGAG | GCCAGAGCGC | CCTGCTGAGC | 120 |
| AACAAAGGAC | TCCTGCAGCC | TTCTCTGTCT | GTCTCTGGC | GCAGGCACAT | GGGGAGGCCT | 180 |
| CCCGCAGGGT | GGGGGCCACC | AGTCCAGGGG | TGGGAGCACT | ACANGGGGTG | GGAGTGGGTG | 240 |
| GTGGCTGGTN | CNAATGGCCT | GNCACANATC | CCTACGATTC | TTGACACCTG | GATTCACCA | 300 |
| GGGGACCTTC | TGTTCTCCA | NGNAACTTC | NTNNATCTCN | AAAGAACACA | ACTGTTTCTT | 360 |
| CNGCANTTCT | GGCTGTTCAT | GGAAAGCACA | GGTGTCCNAT | TTNGGCTGGG | ACTGGTACAA | 420 |
| TATGGTTCCG | GCCCACCTCT | CCCNCTNAAN | AACTATTCA | CCCCCCCCCN | CNTCTNTG | 480 |
| CCTGGGCCCT | TAANTACCCA | CACCGGAAC | CANTTANTTA | TTCATCTTNG | GNTGGGCTTG | 540 |
| NTNNATCNCCN | CCTGAANGCG | CCAAGTTGAA | AGGCCACGCC | GTNCCCCNTC | CCCATAGNAN | 600 |
| NTTTTNNCNT | CANCTAATGC | CCCCCNNGC | AACNATCCAA | TCCCCCCCCN | TGGGGCCCC | 660 |
| AGCCCANGGC | CCCCGNCTCG | GGNNNCNGN | CNCGNANTCC | CCAGGNTCTC | CCANTCNGNC | 720 |
| CNNNGCNCC | CCCGCACGCA | GAACANAAGG | NTNGACCNC | CGCANNNNNN | NGGTNNCNAC | 780 |
| CTCGCCCCCCC | CCNNCGNNG | | | | | 799 |

(2) INFORMATION FOR SEQ ID NO:32:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 789 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

| | | | | | | |
|------------|------------|-------------|-------------|------------|-------------|-----|
| TTTTTTTTT | TTTTTTTTT | TTTTTTTTT | TTTTTTTTT | TTTTTTTTT | TTTTTTTTT | 60 |
| TTTTNNCAG | GGCAGGTTA | TTGACAACCT | CNCGGACAC | AANCAGGCTG | GGGACAGGAC | 120 |
| GGCAACAGGC | TCCGGGGCG | GCGGGCGCG | CCCTACCTGC | GGTACCAAAT | NTGCAGCCTC | 180 |
| CGCTCCCGCT | TGATNTTCT | CTGCAGCTGC | AGGATGCCNT | AAAACAGGGC | CTCGGCCNTN | 240 |
| GTTGGGACC | CTGGGATTN | AATTTCACAG | GGCACAAATGC | GGTCGCANCC | CCTCACCAACC | 300 |
| NATTAGGAAT | AGTGGTNTA | CCCNCCNCCG | TTGGCNCACT | CCCCNTGGAA | ACCACTTNTC | 360 |
| GCGGCTCCGG | CATCTGGTCT | TAAACCTTG | AAACNCTGGG | GCCCTTCTTT | TGGTTANTNT | 420 |
| NCCNGCACA | ATCATNACTC | AGACTGGNC | GGGCTGGCCC | AAAAAAANCN | CCCCAAAACC | 480 |
| GGNCATGTC | TTNNCGGGGT | TGCTGCNATN | TNCATCACCT | CCCGGGCNCA | NCAGGNCAAC | 540 |
| CCAAAAGTTC | TTGNGCCCN | AAAAAAANC | CCGGGGGGNC | CCAGTTTCAA | CAAAGTCATC | 600 |
| CCCCTTGGCC | CCCAAATCCT | CCCCCCGNTT | NCTGGGTTTG | GGAACCCAGC | CCTCTNNCTT | 660 |
| TGGNNGGCAA | GNTGGNTCCC | CTTCGGGCC | CCCGGTGGGC | CCNNCTCTAA | NGAAAACNCC | 720 |
| NTCCTNNCA | CCATCCCCC | NNGNNAACGNC | TANCAANGNA | TCCCTTTTTT | TANAAACGGG | 780 |
| CCCCCCNCG | | | | | | 789 |

(2) INFORMATION FOR SEQ ID NO:33:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 793 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:

| | | | | | | |
|-------------|------------|------------|------------|------------|------------|-----|
| GACAGAACAT | GTTGGATGGT | GGAGCACCTT | TCTATACGAC | TTACAGGACA | GCAGATGGGG | 60 |
| AATTCAATGGC | TGTTGGAGCA | ATANAACCCC | AGTTCTACGA | GCTGCTGATC | AAAGGACTTG | 120 |
| GACTAAAGTC | TGATGAACTT | CCCAATCAGA | TGACCATGGA | TGATTGGCCA | GAAATGAANA | 180 |
| AGAAGTTTGC | AGATGTATTT | GAAAGAAGA | CGAAGGCAGA | GTGGTGTCAA | ATCTTGACG | 240 |
| GCACAGATGC | CTGTGTGACT | CCGGTTCTGA | CTTTTGAGGA | GGTTGTTCAT | CATGATCACA | 300 |

| | | | | | | |
|------------|-------------|------------|------------|------------|------------|-----|
| ACAANGAACG | GGGCTCGTT | ATCACCA | AGGAGCAGGA | CGTGAGCCCC | CGCCCTGCAC | 360 |
| CTCTGCTGTT | AAACACCCCCA | GCCATCCCTT | CTTCAAAAAG | GGATCCACTA | CTTCTAGAGC | 420 |
| GGNCGCCACC | GCGGTGGAGC | TCCAGCTTT | GTTCCCTTA | GTGAGGGTTA | ATTGCGCGCT | 480 |
| TGGCGTAATC | ATGGTCATAN | CTGTTCTG | TGTGAAATTG | TTATCCGCTC | ACAATTCCAC | 540 |
| ACAACATAAG | ANCCCGGAAGC | ATNAATTT | AAAGCTTGGN | GGTNCCTAA | TGANTGAACT | 600 |
| NACTCACATT | AATTGGCTTT | GCGCTCACTG | CCCGCTTCC | AGTCCGGAAA | ACCTGTCCTT | 660 |
| GCCAGCTGCC | NTTAATGAAT | CNGGCCACCC | CCCGGGGAAA | AGGCNGTTIG | CTTNTTGGGG | 720 |
| CGCNCTTCCC | GCTTCTCGC | TTCCTGAANT | CCTTCCCCC | GGTCTTCCG | CTTGCGGCNA | 780 |
| ACGGTATCNA | CCT | | | | | 793 |

(2) INFORMATION FOR SEQ ID NO:34:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 756 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:

| | | | | | | |
|------------|------------|------------|------------|-------------|------------|-----|
| GCCCGCACCG | GCATGTACGA | GCAACTCAAG | GGCGACTGGA | ACCGTAAAAG | CCCCAATCTT | 60 |
| ANCAAGTGGC | GGGAANAGCT | GGGTCGACTC | AAGCTAGTTC | TTCTGGAGCT | CAACTTCTTG | 120 |
| CCAACCACAG | GGACCAAGCT | GACCAAACAG | CAGCTAATT | TGCCCCGTGA | CATACTGGAG | 180 |
| ATCGGGGCC | AATGGAGCAT | CCTACGCAAN | GACATCCCC | CCTTCGAGCG | CTACATGGCC | 240 |
| CAGCTAAAT | GCTACTACTT | TGATTACAA | GAGCAGCTCC | CCGAGTCAGC | CTATATGCAC | 300 |
| CACTCTTGG | GCCTCAACCT | CCTCTTCTG | CTGTCAGA | ACCGGGTGGC | TGANTNCCAC | 360 |
| ACGGANTTGG | ANCGGCTGCC | TGCCCAANGA | CATACANACC | AATGTCTACA | TCNACCACCA | 420 |
| GTGCTCTGGA | GCAAACTGTA | TGGANGGCAG | CTACCNAAA | GTNTTCTGG | CCNAGGGTAA | 480 |
| CATCCCCCGC | CGAGAGCTAC | ACCTTCTCA | TTGACATCCT | GCTCGACACT | ATCAGGGATG | 540 |
| AAAATCGCNG | GGTTGCTCCA | GAAAGGCTNC | AAAANATCC | TTTTCNCTGA | AGGCCCCCGG | 600 |
| ATNCNCTAGT | NCTAGAATCG | GCCGCCATC | GCGGTGGANC | CTCCAAACCTT | TCGTTNCCCT | 660 |
| TTACTGAGGG | TTNATTGCCG | CCCTTGCCTG | TATCATGGTC | ACNCCNGTTN | CCTGTGTTGA | 720 |
| AATTNTTAAC | CCCCCACAAT | TCCACGCCNA | CATTNG | | | 756 |

(2) INFORMATION FOR SEQ ID NO:35:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 834 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:35:

| | | | | | | |
|-------------|------------|------------|------------|------------|------------|-----|
| GGGGATCTCT | ANATCNACCT | GNATGCATGG | TTGTCGGTGT | GGTCGCTGTC | GATGAANATG | 60 |
| AACAGGATCT | TGCCCTTGAA | GCTCTCGGCT | GCTGTNTTTA | AGTTGCTCAG | TCTGCCGTCA | 120 |
| TAGTCAGACA | CNCTCTTGGG | CAAAAAACAN | CAGGATNTGA | GTCTGATTT | CACCTCCAAT | 180 |
| AATCTTCNGG | GCTGTCGCT | CGGTGAACTC | GATGACNANG | GGCAGCTGGT | TGTGTNTGAT | 240 |
| AAANTCCANC | ANGTTCTCCT | TGGTACACTC | CCCTCAAAG | TTGTTCCGGC | CTTCATCAA | 300 |
| CTTCTNNAAAN | ANGANNANCC | CANCTTTGTC | GAGCTGGNAT | TTGGANAACA | CGTCACTGTT | 360 |
| GGAAACTGAT | CCCAAATGGT | ATGTCATCCA | TCGCTCTG | TGCCCTGAAA | AAACTTGCTT | 420 |
| GGCNCAAATC | CGACTCCCCN | TCCTTGAAAG | AAGCCNATCA | CACCCCCCTC | CCTGGACTCC | 480 |
| NNCAANGACT | CTNCCGCTNC | CCCNTCCNN | CAGGGTTGGT | GGCANNCCGG | GCCCNTGCGC | 540 |
| TTCTTCAGCC | AGTTCACNAT | NTTCATCAGC | CCCTCTGCCA | GCTGTTNTAT | TCCTTGGGGG | 600 |
| GGAANCCGTC | TCTCCCTTCC | TGAANNAACT | TTGACCGTNG | GAATAGCCGC | GCNTCNCNT | 660 |
| ACNTNCTGGG | CCGGGTTCAA | ANTCCCTCCN | TTGNCNNTCN | CCTCGGGCCA | TTCTGGATT | 720 |
| NCCNAACTTT | TTCCTTCCCC | CNCCCCNCGG | NGTTGGNTT | TTTCATNGGG | CCCCAACTCT | 780 |

GCTNTTGGCC ANTCCCCTGG GGGCANTNTAN CNCCCCNTNT GGTCCCNNTNG GGCC

834

(2) INFORMATION FOR SEQ ID NO:36:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 814 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:36:

| | | | | | | |
|-------------|-------------|------------|------------|-------------|------------|-----|
| CGGNCGCTTT | CCNGCCGCGC | CCCGTTCCA | TGACNAAGGC | TCCCTTCANG | TTAAATACNN | 60 |
| CCTAGNAAAC | ATTAATGGGT | TGCTCTACTA | ATACATCATA | CNAACCAGTA | AGCCTGCCA | 120 |
| NAACGCCAAC | TCAGGCCATT | CCTACCAAAG | GAAGAAAGGC | TGGTCTCTCC | ACCCCTGTAA | 180 |
| GGAAAGGCCT | GCCTTGTAAG | ACACCACAAT | NCGGCTGAAT | CTNAAGTCTT | GTGTTTTACT | 240 |
| AATGGAAAAAA | AAAATAAAC | AANAGGTTT | GTTCTCATGG | CTGCCACCG | CAGCCTGGCA | 300 |
| CTAAAACANC | CCAGGGCTCA | CTTCTGCTTG | GANAATATT | CTTGCTCTT | TTGGACATCA | 360 |
| GGCTTGATGG | TATCACTGCGC | ACNTTTCCAC | CCAGCTGGGC | NCCCTTCCCC | CATNTTTGTC | 420 |
| ANTGANCTGG | AAGGCCTGAA | NCTTAGTCTC | CAAAGTCTC | NGCCCCACAAG | ACCGGCCACC | 480 |
| AGGGGANGTC | NTTNCAGTG | GATCTGCCAA | ANANTACCCN | TATCATICNT | GAATAAAAAG | 540 |
| GCCCCGTAAC | GANATGCTTC | CANCANCTT | TAAGACCCAT | AATCCTNGAA | CCATGGTGGC | 600 |
| CTTCCGGTCT | GATCCNAAG | GAATGTTCTT | GGGTCCANT | CCCTCCTTTG | TTNCTTACGT | 660 |
| TGTNTTGGAC | CCNTGCTNGN | ATNACCCAN | TGANATCCCC | NGAAGCACC | TNCCCTGGC | 720 |
| ATTGANTTT | CNTAAATTCT | CTGCCCTACN | NCTGAAAGCA | CNATCCCTN | GCCNCCNAAN | 780 |
| GGNGAACTCA | AGAAGGTCTN | NGAAAACCA | CNCN | | | 814 |

(2) INFORMATION FOR SEQ ID NO:37:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 760 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:37:

| | | | | | | |
|------------|------------|-------------|------------|-------------|------------|-----|
| GCATGCTGCT | CTTCCTAAAG | GTTGTTCTTG | TTGCCATAAC | AACCACCAT | GGTAAAGCGG | 60 |
| GCGCAGTGT | CGCTGAAGGG | GTTGAGTAC | CAGCGGGGA | TGCTCTCCTT | GCAGAGTCCT | 120 |
| GTGTCTGGCA | GGTCCACGCA | ATGCCCTTTG | TCACTGGGG | AATGGATGCG | CTGGAGCTCG | 180 |
| TCNAANCCAC | TCGTGTATT | TTCACANGCA | GCCTCTCCG | AAGCNTCCGG | GCAGTTGGGG | 240 |
| GTGTGTCAC | ACTCCACTAA | ACTGTGATN | CANCAAGCCA | TTGCTGCAGC | GGAACTGGGT | 300 |
| GGGCTGACAG | GTGCCAGAAC | ACACTGGATN | GGCCTTCCA | TGGAAGGGCC | TGGGGGAAAT | 360 |
| CNCCTNANCC | CAAACATGCC | CTCAAAGGCC | ACCTTGACAA | CCCCGACAGG | CTAGAAATGC | 420 |
| ACTCTCTTC | CCAAAGGTAG | TTGTTCTTGT | TGCCAAGCA | NCCTCCANCA | AACCAAAANC | 480 |
| TTGCAAAATC | TGCTCCGTGG | GGGTCACTNNN | TACCANGTT | GGGGAAANAA | ACCCGGCNGN | 540 |
| GANCCNCTT | GTTGAATGC | NAAGGNAATA | ATCCTCCTGT | CTTGCTTGGG | TGGAANAGCA | 600 |
| CAATTGAACT | GTAAACNTTG | GGCGCNGTTC | CNCTNGGGTG | GTCGTAAACT | AATCACCGTC | 660 |
| ACTGGAAAAA | GGTANGTGCC | TTCCCTTGAAT | TCCCAAANTT | CCCCNTNGNTT | TGGGTNNNTT | 720 |
| CTCCTCTNCC | CTAAAATCG | TNTTCCCCCC | CCNTANGGCG | | | 760 |

(2) INFORMATION FOR SEQ ID NO:38:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 724 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:38:

| | | | | | |
|-------------|-------------|------------|------------|------------|-----|
| TTTTTTTTTT | TTTTTTTTTT | TTTTAAAAAA | CCCCCTCCAT | TGAATGAAAA | 60 |
| CTTCCNAAT | TGTCCAACCC | CTCNNCCAA | ATNNCCATT | CGGGGGGGG | 120 |
| CAAATTAAATT | TTGGANNTTA | AATTAAATNT | TNATNINGGG | AANAANCCAA | 180 |
| AATTAAACCC | ATTATNAACT | AAATNCTCN | AAACCNTG | GNTCCAAAAA | 240 |
| CTTAAATCCC | TCCGAAATTC | NTAANGAAA | ACCAAATT | CCTAAGGCTN | 300 |
| NGATTTAAAC | CCCCTTNANT | TNTTTNACC | CNNNGCTNAA | NTATTTNGNT | 360 |
| TCCTNTTAAN | CNTNGTAAC | TCCCGNTAAT | GAANNNCCT | AANCAATTAA | 420 |
| TTTTGAATT | GGGAAATTCCN | NGGGATTNA | CGGGGTTTT | TCCCNNTTGG | 480 |
| CCCNCTTCG | GGGTTTGGGN | NTAGGTTGAA | TTTTTNANG | GGGCATNCC | 540 |
| AAAAAACTCC | CAAGNNTAA | TTNGAATNTC | CCCCTCCCA | GGCCTTTGG | 600 |
| TTNTTGGGG | CNNGGGANTT | CNTTCCCCCN | TNCCNNTCCC | GGGGCNGGT | 660 |
| NGNNTTGGT | TTTGGGCC | CTTNANGAC | CTTCCGGATN | AAANGTTAT | 720 |
| | | | | CCCCGGGNCG | 724 |
| | | | | GCCG | |

(2) INFORMATION FOR SEQ ID NO:39:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 751 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:39:

| | | | | | | |
|-------------|------------|------------|--------------|------------|------------|-----|
| TTTTTTTTTT | TTTTCTTTG | CTCACATTTA | ATTTTATT | TGATTTTTT | TAATGCTGCA | 60 |
| CAACACAATA | TTTATTTCAT | TTGTTCTTT | TATTCATT | TATTTGTTG | CTGCTGCTGT | 120 |
| TTTATTATT | TTTACTGAAA | GTGAGAGGGA | ACTTTGTGG | CCTTTTTTCC | TTTTTCTGTA | 180 |
| GGCCGCCTTA | AGCTTCTAA | ATTTGGAACA | TCTAACAGCAAG | CTGAANGGAA | AAGGGGGTTT | 240 |
| CGCAAAATCA | CTCGGGGAA | NGGAAAGGTT | GCTTTGTTAA | TCATGCCCTA | TGGTGGGTGA | 300 |
| TTAACTGCTT | GTACAATTAC | NTTTCAC | TAATTAAATTG | TGCTNAANGC | TTAATTANA | 360 |
| CTTGGGGGTT | CCCTCCCCAN | ACCAACCCN | CTGACAAAAA | GTGCCNGCCC | TCAAATNATG | 420 |
| TCCCGGCNT | CNTGAAACA | CACNGCNGAA | NGTTCTCATT | NTCCCNCCNC | CAGGTNAAA | 480 |
| TGAAGGGTTA | CCATNTTAA | CNCCACCTCC | ACNTGGCENN | GCCTGAATCC | TCNAAAANCN | 540 |
| CCCTCAANCN | AATTNCTNNG | CCCCGGTNC | GCNTRNNGTCC | CNCCCGGGCT | CGGGGAANTN | 600 |
| CACCCCNGA | ANNCNNTNNC | NAACNAATT | CCGAAAATAT | TCCCNNTNC | TCAATTCCCC | 660 |
| CNNAGACTNT | CCTCNCCNAN | CNCAATTTC | TTTNNTCAC | GAACNCGNNC | CNNAAAATGN | 720 |
| NNNNCNCCCTC | CNCTNGTCCN | NAATCNCCAN | C | | | 751 |

(2) INFORMATION FOR SEQ ID NO:40:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 753 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:40:

| | | | | | | |
|------------|------------|------------|------------|------------|-------------|-----|
| GTGGTATTTT | CTGTAAGATC | AGGTGTCCT | CCCTCGTAGG | TTTAGAGGAA | ACACCCCTCAT | 60 |
| AGATGAAAAC | CCCCCCGAGA | CAGCAGCACT | GCAACTGCCA | AGCAGCCGGG | CTAGGAGGGG | 120 |
| CGCCCTATGC | ACAGCTGGGC | CCTTGAGACA | GCAGGGCTTC | GATGTCAGGC | TCGATGTCAA | 180 |

| | | | | | | | |
|------------|------------|------------|------------|------------|------------|------------|-----|
| TGGTCTGGAA | GCGGCGGCTG | TACCTGCGTA | GGGGCACACC | GTCAGGGCCC | ACCAAGGA | ACT | 240 |
| TCTCAAAGTT | CCAGGCAACN | TCGTTGCAC | ACACCGGAGA | CCAGGTGATN | AGCTTGGGT | | 300 |
| CGGTCA | TAAN | CGCGGTGGCG | TCGTCGCTGG | GAGCTGGCAG | GGCCTCCCGC | AGGAAGGCNA | 360 |
| ATAAAAGGTG | CGCCCCCGCA | CCGTTCANCT | CGCACTTCTC | NAANACCATG | ANGTTGGGCT | | 420 |
| CNAACCCACC | ACCAANCCCG | ACTTCCTGA | NGGAATTCCC | AAATCTCTC | GNTCTGGGC | | 480 |
| TTCTNCTGAT | GCCCTANCTG | GTTGCCCN | ATGCCAANCA | NCCCAANCC | CCGGGGTCC | | 540 |
| AAANCACCCN | CCTCCTCNTT | TCATCTGGGT | TNTNTCCCC | GGACCN | TGTTCTCAAG | | 600 |
| GGANCCCATA | TCTCNACCAN | TACTCAC | NTNCCCCNT | GNNA | CCANC | CTTCTANN | 660 |
| TTCCCNCCCG | NCCTCTGGCC | CNTCAAANAN | GCTTNACNA | CCTGGGTCTG | CCTTCCCC | | 720 |
| TNCCCTATCT | GNACCCCN | TTTGTC | TCA | TNT | | | 753 |

(2) INFORMATION FOR SEQ ID NO:41:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 341 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:41:

| | | | | | | | |
|------------|------------|------------|------------|------------|------------|--|-----|
| ACTATATCCA | TCACAACAGA | CATGCTTCAT | CCCATAGACT | TCTTGACATA | GCTTCAAATG | | 60 |
| AGTGAACCCA | TCCTTGATT | ATATACAT | ATGTTCTCAG | TATTTGGGA | GCCTTTCCAC | | 120 |
| TTCCTTAAAC | CTTGTTCATT | ATGAACACTG | AAAATAGGAA | TTTGTGAAGA | GTTAAAAGT | | 180 |
| TATAGCTTGT | TTACGTAGTA | AGTTTTGAA | GTCTACATTC | AATCCAGACA | CTTAGTTGAG | | 240 |
| TGTTAAACTG | TGATTTTAA | AAAATATCAT | TTGAGAATAT | TCTTCAGAG | GTATTTCAT | | 300 |
| TTTTACTTT | TGATTAATTG | TGTTTTATAT | ATTAGGGTAG | T | | | 341 |

(2) INFORMATION FOR SEQ ID NO:42:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 101 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:42:

| | | | | | | | |
|------------|------------|-----------|------------|------------|------------|---|-----|
| ACTTACTGAA | TTTAGTTCTG | TGCTCTCCT | TATTTAGTGT | TGTATCATAA | ATACTTTGAT | | 60 |
| GTTC | AAACA | TA | ATA | TTTCA | GTGGCTTCAT | A | 101 |

(2) INFORMATION FOR SEQ ID NO:43:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 305 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:43:

| | |
|---|-----|
| ACATCTTTGT TACAGTCTAA GATGTGTTCT TAAATCACCA TTCCCTTCCTG GTCTCACCC | 60 |
| TCCAGGGTGG TCTCACACTG TAATTAGAGC TATTGAGGAG TCTTACAGC AAATTAAGAT | 120 |
| TCAGATGCCT TGCTAAGTCT AGAGTTCTAG AGTTATGTTT CAGAAAGTCT AAGAAACCCA | 180 |
| CCTCTTGAGA GGTCAGTAAA GAGGACTTAA TATTTCATAT CTACAAAATG ACCACAGGAT | 240 |
| TGGATACAGA ACAGAGAGTTA TCCTGGATAA CTCAGAGCTG AGTACACTGCC CGGGGGCCGC | 300 |
| TCGAA | 305 |

(2) INFORMATION FOR SEQ ID NO:44:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 852 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:44:

| | |
|--|-----|
| ACATAAAATAT CAGAGAAAAG TAGTCTTGAA AATATTTACG TCCAGGAGTT CTTTGTCT | 60 |
| GATTATTTGG TGTGTGTTT GGTTTGTGTC CAAAGTATTG GCAGCTTCAG TTTTCATTTC | 120 |
| CTCTCCATCC TCGGGCATTC TTCCCAAATT TATATACCAG TCTTCGTCCA TCCACACGCT | 180 |
| CCAGAATTTC TCTTTTGAG TAATATCTCA TAGCTCGGCT GAGCTTTCA TAGTCATGC | 240 |
| TGCTGTTGTT CTTCTTTTTA CCCATAGCT GAGCCACTGTC CTCTGATTTA AAGAACCTGA | 300 |
| AGACGCCCTC AGATCGGCTC TCCCATTAA TTAATCCTGG GTTCTTGTCT GGGTTCAAGA | 360 |
| GGATGTCGCG GATGAATTCC CATAAGTGAG TCCCTCTCGG GTTGTGCTTT TTGGTGTGGC | 420 |
| ACTTGGCAGG GGGGTCTTGC TCCTTTTCATA TATCAGGTGA CTCTGCAACA GGAAGGTGAC | 480 |
| TGGTGGTTGT CATGGAGATC TGAGCCCGGC AAAAAGTTT GCTGTCCAAC AAATCTACTG | 540 |
| TGCTTACCAATA GTTGGTGTCA TATAAATAGT TCTNGTCTTT CCAGGTGTTTC ATGATGGAAG | 600 |
| GCTCAGTTTG TTCAGTCTTG ACAATGACAT TGTGTGTGGA CTGGAACAGG TCACTACTGC | 660 |
| ACTGGCCGTT CCACCTTCAGA TGCTGCAAGT TGCTGTAGAG GAGNTGCCCG GCCGTCCCTG | 720 |
| CCGCCCGGGT GAACTCCTGC AAACATCATGC TGCAAAGGTG CTCGCCGTTG ATGTCGAAC | 780 |
| CNTGGAAAGG GATACAATTG GCATCCAGCT GGTTGGTGTCA CAGGAGGTGA TGGAGCCACT | 840 |
| CCACACACTG GT | 852 |

(2) INFORMATION FOR SEQ ID NO:45:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 234 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:45:

| | |
|--|-----|
| ACACAGACCC TTGCTCGCT AACGACCTCA TGCTCATCAA GTTGGACGAA TCCGTGTCGG | 60 |
| AGTCTGACAC CATCGGGAGC ATCAGGATTG CTTCGAGTG CCCTACCGCG GGGAACTCTT | 120 |
| GCCTCGTTTC TGGCTGGGGT CTGCTGGCGA ACGGCAGAAT GCCTACCGTG CTGCAGTGC | 180 |

TGAACGTGTC GGTGGTGTCT GAGGAGGTCT GCAGTAAGCT CTATGACCCG CTGT

234

(2) INFORMATION FOR SEQ ID NO:46:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 590 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:46:

| | |
|---|-----|
| ACTTTTATT TAAATGTTTA TAAGGCAGAT CTATGAGAAT GATAGAAAAC ATGGTGTGTA | 60 |
| ATTGATAGC AATATTTGG AGATTACAGA GTTTAGTAA TTACCAATT CACAGTTAA | 120 |
| AAGAAGATAA TATATTCCA GCANATACAA AATATCTAA GAAAGATCAA GGCAGGAAA | 180 |
| TGANTATAAC TAATTGACAA TGGAAAATCA ATTTTAATGT GAATTGCACA TTATCCTTTA | 240 |
| AAAGCTTTCA AAANAAANAA TTATTGCAGT CTANTTAATT CAAACAGTGT TAAATGGTAT | 300 |
| CAGGATAAAAN AACTGAAGGG CANAAAGAAT TAATTTTCAC TTCACTGAAAC NCACCCANAT | 360 |
| TTACAATGGC TTAATGCAN GGAAAAGCA GTGGAAGTAG GGAAGTANTC AAGGTCTTTC | 420 |
| TGGCTCTAA TCTGCCTTAC TCTTGGGTG TGGCTTGAT CCTCTGGAGA CAGCTGCCAG | 480 |
| GGCTCCTGTT ATATCCACAA TCCCAGCAGC AAGATGAAGG GATGAAAAAG GACACATGCT | 540 |
| GCCTCCCTT GAGGAGACTT CATCTCACTG GCCAACACTC AGTCACATGT | 590 |

(2) INFORMATION FOR SEQ ID NO:47:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 774 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:47:

| | |
|--|-----|
| ACAAGGGGGC ATAATGAAGG AGTGGGGANA GATTTAAAG AAGGAAAAAAA AACGAGGCC | 60 |
| TGAACAGAAAT TTCTCTGNAC AACGGGGCTT CAAAATAATT TTCTGGGGA GGTCAAGAC | 120 |
| GCTTCACTGC TTGAAACTTAA AATGGATGTG GGACANAATT TTCTGTAATG ACCCTGAGGG | 180 |
| CATTACAGAC GGGACTCTGG GAGGAAGGAT AAACAGAAAG GGGACAAAGG CTAATCCCAA | 240 |
| AAACATCAAAG AAAGGAAGGT GGCCTCATAC CTCCCAGCCT ACACAGTTCT CCAGGGCTCT | 300 |
| CCTCATCCCT GGAGGACGAC AGTGGAGGAA CAACTGACCA TGCCCCCAGG CTCTGTGTG | 360 |
| CTGGCTCTTG GTCTTCAGCC CCCAGCTCTG GAAGCCCACC CTCTGCTGAT CCTGCGTGGC | 420 |
| CCACACTCCT TGAACACACA TCCCCAGGTT ATATTCCCTGG ACATGGCTGA ACCTCCTATT | 480 |
| CCTACTTCCG AGATGCCTTG CTCCCTGCAG CCTGTCAAAA TCCCACTCAC CCTCCAAACC | 540 |
| ACGGCATGGG AAGCCTTCT GACTTGCTG ATTACTCCAG CATCTTGAA CAATCCCTGA | 600 |
| TTCCCCACTC CTTAGAGGCA AGATAGGGTG GTTAAGAGTA GGGCTGGACC ACTTGGAGCC | 660 |
| AGGCTGCTGG CTTCAAATTN TGGCTCATTT ACGAGCTATG GGACCTTGGG CAAGTNATCT | 720 |
| TCACCTCTAT GGGCNTCATT TTGTTCTACC TGCAAAATGG GGGATAATAA TAGT | 774 |

(2) INFORMATION FOR SEQ ID NO:48:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 124 base pairs

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:48:

| | |
|--|-----|
| CANAAATTGAA ATTTTATAA AAAGGCATTT TTCTCTTATA TCCATAAAAT GATATAATT | 60 |
| TTCGAANTAT ANAAATGTGT CATAAATTAT AATGTTCTT ATTACAGCT CAACGCAACT | 120 |
| TGGT | 124 |

(2) INFORMATION FOR SEQ ID NO:49:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 147 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:49:

| | |
|--|-----|
| GCCGATGCTA CTATTTATT GCAGGGAGGTG GGGGTGTTT TATTATTCTC TCAACAGCTT | 60 |
| TGTGGCTACA GGTGGTGTCT GACTGCATNA AAAANTTTT TACGGGTGAT TGCAAAAATT | 120 |
| TTAGGGCACC CATATCCCAA GCANTGT | 147 |

(2) INFORMATION FOR SEQ ID NO:50:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 107 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:50:

| | |
|--|-----|
| ACATTAATT AATAAAAGGA CTGTTGGGT TCTGCTAAA CACATGGCTT GATATATTGC | 60 |
| ATGGTTTGAG GTTAGGAGGA GTTAGGCATA TGTTTGGGA GAGGGGT | 107 |

(2) INFORMATION FOR SEQ ID NO:51:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 204 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:51:

| | |
|---|-----|
| GTCCTAGGAA GTCTAGGGGA CACACGACTC TGGGGTCACG GGGCCGACAC ACTTGCACGG | 60 |
| CGGGAAGGAA AGGCAGAGAA GTGACACCGT CAGGGGAAA TGACAGAAAG GAAAATCAAG | 120 |
| GCCTTGCAAG GTCAGAAAGG GGACTCAGGG CTTCCACCAC AGCCCTGCCA CACTTGGCCA | 180 |
| CCTCCCTTTT GGGACCAGCA ATGT | 204 |

(2) INFORMATION FOR SEQ ID NO:52:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 491 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:52:

| | |
|--|-----|
| ACAAAGATAA CATTATCTT ATAACAAAAAA TTGATAGTT TAAAGGTTA GTATTGTGTA | 60 |
| GGGTATTTT CAAAAGACTA AAGAGATAAC TCAGTAAAAA AGTTAGAAAT GTATAAAACA | 120 |
| CCATCAGACA GGTTTTTAAA AAACAACATA TTACAAAATT AGACAATCAT CCTTAAAAAA | 180 |
| AAAACCTTCTT GTATCAATT CTGGTCA AAAAGCTGA CTTAANTATT TTTAAATATT | 240 |
| TCANAAACAC TTCCTCAAAA ATTTCAANA TGGTAGCTTT CANATGTNCC CTCAGTCCCA | 300 |
| ATGTTGCTCA GATAAAATATAA TCTCGTGAGA ACTTACCAACC CACCACAAAGC TTTCTGGGC | 360 |
| ATGCAACAGT GTCTTTCTT TNCTTTCTT TTTTTTTTTT TTACAGGCAC AGAAACTCAT | 420 |
| CAATTTATT TGGATAACCAA AGGGTCTCCA AATTATATTG AAAAATAAAT CCAAGTTAAT | 480 |
| ATCACTCTTG T | 491 |

(2) INFORMATION FOR SEQ ID NO:53:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 484 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:53:

| | |
|---|-----|
| ACATAATTTA GCAGGGCTAA TTACCATAG ATGCTATTTA TAAANAGGTN TATGATCTGA | 60 |
| GTATTAACAG TTGCTGAAGT TTGGTATTTT TATGCAGCAT TTTCTTTTG CTTTGATAAC | 120 |
| ACTACAGAAC CCTTAAGGAC ACTGAAAATT AGTAAGTAA GTTCAGAAC ATTAGCTGCT | 180 |
| CAATCAAATC TCTACATAAC ACTATAGTAA TAAACACGTT AAAAAAAAGT GTTGAATCT | 240 |
| GCACCTAGTAT ANACCGCTCC TGTCAAGGATA ANACTGCTTT GGAACAGAAA GGGAAAAANC | 300 |
| ACCTTTGANT TTCTTTGTC TGATANGAGG AAAGGCTGAA TTACCTTGTG GCCTCTCCCT | 360 |
| AATGATTGGC AGGTCNGGTA AATNCCAAA CATATTCAA CTCACACCTT CTTTCCNCG | 420 |
| TANCTTGANT CTGTGTATTC CAGGANCAGG CGGATGGAAT GGGCCAGCCC NCGGATGTC | 480 |
| CANT | 484 |

(2) INFORMATION FOR SEQ ID NO:54:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 151 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:54:

| | |
|--|-----|
| ACTAAACCTC GTGCTTGTA ACTCCATACA GAAAACGGTG CCATCCCTGA ACACGGCTGG | 60 |
| CCACTGGGTA TACTGCTGAC AACCGCAACA ACAAAAAACAC AAATCCTTGG CACTGGCTAG | 120 |
| TCTATGTCT CTCAAAGTGCC TTTTTGTTTG T | 151 |

(2) INFORMATION FOR SEQ ID NO:55:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 91 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:55:

| | |
|---|----|
| ACCTGGCTTG TCTCCGGGTG GTTCCCCGGC CCCCCCACGG TCCCCAGAAC GGACACTTTC | 60 |
| GCCCTCCAGT GGATACTCGA GCCAAAGTGG T | 91 |

(2) INFORMATION FOR SEQ ID NO:56:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 133 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:56:

| | |
|--|-----|
| GGCGGGATGTG CGTTGGTTAT ATACAAATAT GTCATTAT GTAAGGGACT TGAGTATACT | 60 |
| TGGATTTTG GTATCTGTGG GTTGGGGGA CGGTCCAGGA ACCAATACCC CATGGATACC | 120 |
| AAGGGACAAAC TGT | 133 |

(2) INFORMATION FOR SEQ ID NO:57:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 147 base pairs
 - (B) TYPE: nucleic acid

(C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:57:

| | |
|--|-----|
| ACTCTGGAGA ACCTGAGCCG CTGCTCCGCC TCTGGATGA GGTGATGCAN GCNGTGGCCG | 60 |
| GACTGGAGC TGAGCCCTTC CCTTGCGGCC TGCCTCAGAG GATTGTTGCC GACNTGCANA | 120 |
| TCTCANTGGG CTGGATNCAT GCAGGGT | 147 |

(2) INFORMATION FOR SEQ ID NO:58:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 198 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:58:

| | |
|--|-----|
| ACAGGGATAT AGGTTTNAAG TTATTGTNAT TGAAAATAC ATTGAATTTC CTGTATACTC | 60 |
| TGATTACATA CATTATCCT TTAAAAAAGA TGAAATCTT AATTTTATG CCATCTATTA | 120 |
| ATTTACCAAT GAGTTACCTT GTAAATGAGA AGTCATGATA GCACTGAATT TAACTAGTT | 180 |
| TTGACTTCTA AGTTGGT | 198 |

(2) INFORMATION FOR SEQ ID NO:59:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 330 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:59:

| | |
|---|-----|
| ACAACAAATG GGTTGTGAGG AAGTCTTATC AGCAAAACTG GTGATGGCTA CTGAAAAGAT | 60 |
| CCATTGAAAA TTATCATTAA TGATTTAAA TGACAAGTTA TCAAAAACTC ACTCAATTTC | 120 |
| CACCTGTGCT AGCTTGCTAA AATGGGAGTT AACTCTAGAG CAAATATAGT ATCTTCTGAA | 180 |
| TACAGTCAAT AAATGACAAA GCCAGGGCCT ACAGGTGGTT TCCAGACTTT CCAGACCCAG | 240 |
| CAGAAGGAAT CTATTTTATC ACATGGATCT CCGTCTGTGC TCAAAATACC TAATGATATT | 300 |
| TTTCGTCTTT ATTGGACTTC TTTGAAGAGT | 330 |

(2) INFORMATION FOR SEQ ID NO:60:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 175 base pairs
 (B) TYPE: nucleic acid

(C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:60:

| | |
|---|-----|
| ACCGTGGGTG CCTTCTACAT TCCTGACGGC TCCTTCACCA ACATCTGGTT CTACTTCGGC | 60 |
| GTCGTGGCT CCTTCCTCTT CATCCTCATC CAGCTGGTGC TGCTCATCGA CTTTGCGCAC | 120 |
| TCCCTGGAACC AGCGGTGGCT GGGCAAGGCC GAGGAGTGC ATTCCCGTGC CTGGT | 175 |

(2) INFORMATION FOR SEQ ID NO:61:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 154 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:61:

| | |
|---|-----|
| ACCCCACTTT TCCTCCTGTG AGCAGTCTGG ACTTCTCACT GCTACATGAT GAGGGTGAGT | 60 |
| GGTTGTTGCT CTTCAACAGT ATCCTCCCCT TTCCGGATCT GCTGAGCCGG ACAGCAGTGC | 120 |
| TGGACTGCAC AGCCCCGGGG CTCCACATTG CTGT | 154 |

(2) INFORMATION FOR SEQ ID NO:62:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 30 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:62:

| | |
|----------------------------------|----|
| CGCTCGAGCC CTATAGTGAG TCGTATTAGA | 30 |
|----------------------------------|----|

(2) INFORMATION FOR SEQ ID NO:63:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 89 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:63:

| | |
|--|----|
| ACAAGTCATT TCAGCACCC TTGCTTCA AACTGACCA TCTTTATAT TTAATGCTTC | 60 |
| CTGTATGAAT AAAATGGTT ATGTCAAGT | 89 |

(2) INFORMATION FOR SEQ ID NO:64:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 97 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:64:

| | |
|---|----|
| ACCGGAGTAA CTGAGTCGGG ACGCTGAATC TGAATCCACC AATAAATAAA GGTTCTGCAG | 60 |
| AATCAGTGCA TCCAGGATTG GTCCTTGGAT CTGGGGT | 97 |

(2) INFORMATION FOR SEQ ID NO:65:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 377 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:65:

| | |
|---|-----|
| ACAACAANAA NTCCCTTCTT TAGGCCACTG ATGGAACCT GGAACCCCT TTTGATGGCA | 60 |
| GCATGGCGTC CTAGGCCTTG ACACAGCGGC TGGGTTGG GCTNTCCAA ACCGCACACC | 120 |
| CCAACCCTGG TCTACCCACA NTTCTGGCTA TGGGCTGTCT CTGCCACTGA ACATCAGGGT | 180 |
| TGGTCTATAA NATGAAATCC CAANGGGAC AGAGTCAGT AGAGGAAGCT CAATGAGAAA | 240 |
| GCTCAGGCCAG AAAACAGCTG CCTGGCATTC GCCGCTGAAC TATGAACCCG | 300 |
| TGGGGGTGAA CTACCCCCAN GAGGAATCAT GCCTGGGGGA TGCAANGGTG CCAACAGGAG | 360 |
| GGCGGGGAGG AGCATGT | 377 |

(2) INFORMATION FOR SEQ ID NO:66:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 305 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:66:

| | |
|---|-----|
| ACGCCTTTCC CTCAGAATTC AGGGAAAGAGA CTGTCGCCTG CCTTCCTCCG TTGTTGCGTG | 60 |
| AGAACCCGTG TGCCCCCTTCC CACCATATCC ACCCTCGCTC CATCTTGAA CTCAAACACG | 120 |
| AGGAACAAAC TGCACCCCTGG TCCTCTCCCC AGTCCCCAGT TCACCCCTCCA TCCCTCACCT | 180 |
| TCCCTCACTC TAAGGGATAT CAACACTGCC CAGCACAGGG GCCCTGAATT TATGTGGTTT | 240 |
| TTATATATTT TTTAATAAGA TGCACTTTAT GTCATTTTT AATAAAGTCT GAAGAATTAC | 300 |
| TGTTT | 305 |

(2) INFORMATION FOR SEQ ID NO:67:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 385 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:67:

| | |
|---|-----|
| ACTACACACA CTCCACTTGC CCTTGTGAGA CACTTGTCC CAGCACTTTA GGAATGCTGA | 60 |
| GCTGGACCA GCCACATCTC ATGTGCAAGA TTGCCAGCA GACATCAGGT CTGAGAGTTC | 120 |
| CCCTTTAAA AAAGGGGACT TGCTTAAAAA AGAAGTCTAG CCACGATTGT GTAGAGCAGC | 180 |
| TGTGCTGTGC TGAGGATTCA CTTTGAGAG AGTTCTCTC TGAGACCTGA TCTTTAGAGG | 240 |
| CTGGGCAGTC TTGCACATGA GATGGGGCTG GTCTGATCTC AGCACTCCTT AGTCTGCTTG | 300 |
| CCTCTCCCAAG GGCCCCAGCC TGGCCACACC TGCTTACAGG GCACTCTCAG ATGCCATAC | 360 |
| CATAGTTCT GTGCTAGTGG ACCGT | 385 |

(2) INFORMATION FOR SEQ ID NO:68:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 73 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:68:

| | |
|---|----|
| ACTTAAACCAG ATATATTTT ACCCCAGATG GGGATATTCT TTGTAAAAAA TGAAAATAAA | 60 |
| GTTTTTTAA TGG | 73 |

(2) INFORMATION FOR SEQ ID NO:69:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 536 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Homo sapiens*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:69:

| | | | | | | |
|------------|------------|------------|------------|-------------|-------------|-----|
| ACTAGTCCAG | TGTGGTGGAA | TTCCATTGTG | TTGGGGCTC | TCACCCCTCCT | CTCCTGCAGC | 60 |
| TCCAGCTTT | TGCTCTGCCT | CTGAGGAGAC | CATGCCAG | CATCTGAGTA | CCCTGCTGCT | 120 |
| CCTGCTGGCC | ACCCTAGCTG | TGGCCCTGGC | CTGGAGCCCC | AAGGAGGAGG | ATAGGATAAT | 180 |
| CCCGGGTGGC | ATCTATAACG | CAGACCTAA | TGATGAGTGG | GTACAGCGTG | CCCTTCACIT | 240 |
| CGCCATCAGC | GAGTATAACA | AGGCCACCAA | AGATGACTAC | TACAGACGTC | CGCTGCGGGT | 300 |
| ACTAAGAGCC | AGGCAACAGA | CCGTTGGGG | GGTGAATTAC | TTCTTCGACG | TAGAGGTGG | 360 |
| CCGAACCATA | TGTACCAAGT | CCCAGCCAA | CTTGACACC | TGTGCCTTC | ATGAACAGCC | 420 |
| AGAACTGCAG | AAGAACAGT | TGTGCTCTT | CGAGATCTAC | GAAGTCCCT | GGGGAGAACAA | 480 |
| GAANGTCCCT | GGGTGAAATC | CAGGTGTCAA | GAAATCCTAN | GGATCTGTTG | CCAGGC | 536 |

(2) INFORMATION FOR SEQ ID NO:70:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 477 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Homo sapiens*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:70:

| | | | | | | |
|------------|-------------|------------|-------------|-------------|------------|-----|
| ATGACCCCTA | ACAGGGGCC | TCTCAGCCCT | CCTAATGACC | TCCGGCCTAG | CCATGTGATT | 60 |
| TCACTTCCAC | TCCATAACGC | TCCTCATACT | AGGCCTACTA | ACCAACACAC | TAACCATATA | 120 |
| CCAATGATGG | CGCGATGTA | CACGAGAAAG | CACATACCAA | GGCCACCCACA | CACCACCTGT | 180 |
| CCAAAAGGC | CTTCGATAACG | GGATAATCCT | ATTTATTACCC | TCAGAAGTTT | TTTTCTTCGC | 240 |
| AGGGATTTT | CTGAGCCTT | TACCACTCA | GCCTAGCCCC | TACCCCCCAA | CTAGGAGGGC | 300 |
| ACTGGCCAAA | AACAGGCATC | ACCCCGCTAA | ATCCCCCTAGA | AGTCCCCTAC | CTAAACACAT | 360 |
| CGGTATTACT | CGCATCAGGA | GTATCAATCA | CCTGAGCTCA | CCATAGTCTA | ATAGAAAACA | 420 |
| ACCGAAACCA | AATTATTCAA | AGCACTGCTT | ATTACAATTT | TACTGGGTCT | CTATTTT | 477 |

(2) INFORMATION FOR SEQ ID NO:71:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 533 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Homo sapiens*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:71:

| | | | | | | |
|------------|------------|-------------|------------|------------|------------|-----|
| AGAGCTATAG | GTACAGTGTG | ATCTCAGCTT | TGCAAACACA | TTTTCTACAT | AGATAGTACT | 60 |
| AGGTATTAAT | AGATATGAA | AGAAAGAAAT | CACACCATTA | ATAATGGTAA | GATTGGTTA | 120 |
| TGTGATTTA | GTGGTATTTT | TGGCACCCCTT | ATATATGTTT | TCCAAACTTT | CAGCAGTGT | 180 |
| ATTATTTCCA | TAACTTAAA | AGTGAGTTG | AAAAAGAAAA | TCTCCAGCAA | GCATCTCATT | 240 |
| TAAATAAAGG | TTTGTCATCT | TTAAAAATAC | AGCAATATGT | GACTTTTAA | AAAAGCTGTC | 300 |
| AAATAGGTGT | GACCTACTA | ATAATTATTA | GAAATACATT | AAAAACATC | GAGTACCTCA | 360 |
| AGTCAGTTTG | CCTGAAAAAA | TATCAAATAT | AACTCTTAGA | GAAATGTACA | TAAGAGAATG | 420 |
| CTTCGTAATT | TTGGAGTANG | AGGTTCCCTC | CTCAATTTCG | TATTTTAAA | AASTACATGG | 480 |

TAAAAAAAAA AATTACACAAC AGTATATAAG GCTGTAAAAT GAAGAATTCT GCC 533

(2) INFORMATION FOR SEQ ID NO:72:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 511 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:72:

| | | | | | | |
|------------|------------|------------|-------------|------------|-------------|-----|
| TATTACGGAA | AAACACACCA | CATAATTCAA | CTANCAAAGA | ANACTGCTTC | AGGGCGTGTAA | 60 |
| AAATGAAAGG | CTTCCAGGCA | GTTATCTGAT | AAAAAGAACAC | AAAAGAGGG | ACAAGGCTAA | 120 |
| AAGCCGCAGG | ATGTCTACAC | TATANCAGGC | GCTATTTGGG | TTGGCTGGAG | GAGCTGTGGA | 180 |
| AAACATGGAN | AGATTGGTGC | TGGANATCGC | CGTGGCTATT | CCTCATTGTT | ATTACANAGT | 240 |
| GAGGTTCTCT | GTGTGCCAAC | TGGTTGAAA | ACCGTTCTNC | AATAATGATA | GAATAGTACA | 300 |
| CACATGAGAA | CTGAAATGGC | CCAAACCCAG | AAAGAAAGCC | CAACTAGATC | CTCAGAANAC | 360 |
| GCTTCTAGGG | ACAATAACCG | ATGAAGAAAA | GATGGCCTCC | TTGTGCCCCC | GTCTGTTATG | 420 |
| ATTCTCTCC | ATTGCAGCNA | NAAACCCGTT | CTTCTAAGCA | AACNCAGGTG | ATGATGGCNA | 480 |
| AAATACACCC | CCTCTTGAAG | NACCNGGAGG | A | | | 511 |

(2) INFORMATION FOR SEQ ID NO:73:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 499 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:73:

| | | | | | | |
|------------|------------|-------------|------------|------------|------------|-----|
| CAGTGCCAGC | ACTGGTGCCA | GTACCAAGTAC | CAATAACAGT | GCCAGTGCCA | GTGCCAGCAC | 60 |
| CAGTGGTGGC | TTCAGTCTG | GTGCCAGCCT | GACCGCCACT | CTCACATTG | GGCTCTTCGC | 120 |
| TGGCCTTGGT | GGAGCTGGTG | CCAGCACCAG | TGGCAGCTCT | GGTGCCTGTG | GTTTCTCCTA | 180 |
| CAAGTGAGAT | TTTAGATATT | GTTAACCTCTG | CCAGCTTTTC | TCTTCAAGCC | AGGGTGCATC | 240 |
| CTCAGAAACC | TACTCAACAC | AGCACTCTAG | GCAGCCACTA | TCAATCAATT | GAAGTTGACA | 300 |
| CTCTGCATTA | AATCTATTG | CCATTCTGA | AAAAAAAAAA | AAAAAAAGGG | CGGCCGCTCG | 360 |
| ANTCTAGAGG | GCCCCTTAA | ACCCGCTGAT | CAGCCTCGAC | TGTGCCCTCT | ANTTGCAGC | 420 |
| CATCTGTTGT | TTGCCCTTCC | CCCGNTGCT | TCCTTGACCC | TGGAAAGTGC | CACTCCCACT | 480 |
| GTCCTTCCCT | AANTAAAAT | | | | | 499 |

(2) INFORMATION FOR SEQ ID NO:74:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 537 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:74:

| | | | | | | |
|------------|------------|------------|------------|------------|------------|-----|
| TTTCATAGGA | GAACACACTG | AGGAGATACT | TGAAGAATT | GGATTCA | GCCAGAGAT | 60 |
| TTATCAGCTT | AACTCAGATA | AAATCATG | AAGTAATAAG | GTAAAAGCTA | GTCTCTAA | 120 |
| TCCAGGCCA | CGGCTCAAGT | GAATTTGAAT | ACTGCATT | CAGTGAGAG | TAACACATAA | 180 |
| CATTGTATGC | ATGGAAACAT | GGAGGAACAG | TATTACAGTG | TCTTACCACT | CTAATCAAGA | 240 |
| AAAGAATTAC | AGACTCTGAT | TCTACAGTG | TGATTGAATT | CTAAAATGG | TAATCATTAG | 300 |
| GGCTTTGAT | TTATAANACT | TTGGGTACTT | ATACTAAATT | ATGGTAGTTA | TACTGCCCTC | 360 |
| CAGTTTGCTT | GATATATTG | TTGATATTAA | GATTCTTGAC | TTATATTTG | AATGGGTTCT | 420 |
| ACTAAAAAAN | GAATGATATA | TTCTTGAGA | CATCGATATA | CATTATTTA | CACTCTTGAT | 480 |
| TCTACAATGT | AGAAAATGAA | GGAAAATGCC | CAAATTGTAT | GGTGATAAAA | GTCCCGT | 537 |

(2) INFORMATION FOR SEQ ID NO:75:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 467 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:75:

| | | | | | | |
|-------------|------------|------------|------------|-------------|------------|-----|
| CAAANACAAAT | TGTTCAAAAG | ATGCAAATGA | TACACTACTG | CTGCAGCTCA | CAAACACCTC | 60 |
| TGCATATTAC | ACGTACCTCC | TCCTGCTCCT | CAAGTAGTGT | GGTCTATTTT | GCCATCATCA | 120 |
| CCTGCTGTCT | GCTTAGAAGA | ACGGCTTTCT | GCTGCAANGG | AGAGAAATCA | TAACAGACGG | 180 |
| TGGCACAAAG | AGGCCATCTT | TTCCTCATCG | GTTATTGTCC | CTAGAACGCGT | CTTCTGAGGA | 240 |
| TCTAGTTGGG | CTTTCTTCT | GGGTTGGG | CATTCACTT | CTCATGTGTG | TACTATTCTA | 300 |
| TCATTATTGT | ATAACGGTT | TCAAACCNGT | GGGCACNCAG | AGAACCTCAC | TCTGTAATAA | 360 |
| CAATGAGGAA | TAGCCACGGT | GATCTCCAGC | ACCAAATCTC | TCCATGTTNT | TCCAGAGCTC | 420 |
| CTCCAGCCAA | CCCAAATAGC | CGCTGCTATN | GTGTAGAAC | TCCCTGN | | 467 |

(2) INFORMATION FOR SEQ ID NO:76:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:76:

| | | | | | | |
|------------|------------|------------|-------------|------------|------------|-----|
| AAGCTGACAG | CATTGGGCC | GAGATGTCTC | GCTCCGTGGC | CTTAGCTGTG | CTCGCGCTAC | 60 |
| TCTCTCTTTC | TGGCCTGGAG | GCTATCCAGC | GTACTCCAAA | GATTCAAGTT | TACTCACGTC | 120 |
| ATCCAGCAGA | GAATGGAAAG | TCAAATTCC | TGAATTGCTA | TGTGTCTGGG | TTTCATCCAT | 180 |
| CCGACATTGA | AGTTGACTTA | CTGAAGAATG | GAGAGAGAAAT | TGAAAAAGTG | GAGCATTCA | 240 |
| ACTTGTCTTT | CAGCAAGGAC | TGGCTTTCT | ATCTCTTGTA | CTACACTGAA | TTCACCCCCA | 300 |
| CTGAAAAGA | TGAGTATGCC | TGCCGTGTGA | ACCATGTGAC | TTTGTACAG | CCCAAGATNG | 360 |

TTNAGTGGGA TCGANACATG TAAGCAGCAN CATGGGAGGT

400

(2) INFORMATION FOR SEQ ID NO:77:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 248 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: Homo Sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:77:

| | |
|---|-----|
| CTGGAGTGCC TTGGTGTTC AAGCCCCTC AGGAAGCAGA ATGCACCTTC TGAGGCACCT | 60 |
| CCAGCTGCC CGGGGGGGGA TGCGAGGCTC GGAGCACCCCT TGCCCGGCTG TGATTGCTGC | 120 |
| CAGGCAGTGT TCATCTCAGC TTTCTGTCC CTTGCTCCC GGCAAGCGCT TCTGCTGAA | 180 |
| GTTCATATCT GGAGCCTGAT GTCTAACGA ATAAAGGTCC CATGCTCCAC CCGAAAAAAA | 240 |
| AAAAAAAAA | 248 |

(2) INFORMATION FOR SEQ ID NO:78:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 201 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:78:

| | |
|---|-----|
| ACTAGTCCAG TGTGGTGGAA TTCCATTGTG TTGGGCCAA CACAATGGCT ACCTTTAACAA | 60 |
| TCACCCAGAC CCCGCCCTGC CGGTGCCCA CGCTGCTGCT AACGACAGTA TGATGCTTAC | 120 |
| TCTGCTACTC GGAAACTATT TTTATGTAAT TAATGTATGC TTTCTTGTTT ATAAATGCCT | 180 |
| GATTTAAAAA AAAAAAAAAA A | 201 |

(2) INFORMATION FOR SEQ ID NO:79:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 552 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:79:

| | |
|---|-----|
| TCCTTTGTT AGGTTTTGAA GACAACCTA GACCTAAACT GTGTCACAGA CTTCTGAATG | 60 |
| TTAGGCAGT CCTAGTAATT TCCTCGTAAT GATTCTGTTA TTACTTTCT ATTCTTATT | 120 |
| CCTCTTCTT CTGAAGATTA ATGAAGTTGA AAATTGAGGT GGATAAATAC AAAAGGTAG | 180 |

| | |
|---|-----|
| TGTGATAGTA TAAGTATCTA AGTCAGATG AAAGTGTGTT ATATATATCC ATTCAAAATT | 240 |
| ATGCAAGTTA GTAATTACTC AGGGTTAACT AAATTACTTT AATATGCTGT TGAACCTACT | 300 |
| CTGTCCTTG GCTAGAAAAA ATTATAAACCA GGACTTTGTT AGTTGGGAA GCCAAATTGA | 360 |
| TAATATTCTA TGTTCTAAAAA GTTGGGCTAT ACATAAANTA TNAAGAAATA TGGAATTTA | 420 |
| TTCCAGGAA TATGGGTTCA ATTTATGAAT ANTACCGGG ANAGAAGTT TGANTNAAAC | 480 |
| CNGTTTGTT TAATACGTTA ATATGCTTN AATNAACAAG GCNTGACTTA TTCCAAAAAA | 540 |
| AAAAAAAAAA AA | 552 |

(2) INFORMATION FOR SEQ ID NO:80:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 476 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:80:

| | |
|---|-----|
| ACAGGGATTG GAGATGCTAA GGCCCCAGAG ATCGTTGAT CCAACCCCTCT TATTTTCAGA | 60 |
| GGGGAAATG GGGCCTAGAA GTTACAGAGC ATCTAGCTGG TGCGCTGGCA CCCCTGGCCT | 120 |
| CACACAGACT CCCGAGTAGC TGGGACTACA GGCACACAGT CACTGAAGCA GGCCCTGTTT | 180 |
| GCAATTCA CG TTGCCACCTC CAACTTAAC ATTCTTCATA TGTGATGTCC TTAGTCACTA | 240 |
| AGTTAAACT TTCCCACCCA GAAAAGGCAA CTTAGATAAA ATCTTAGAGT ACTTTCATAC | 300 |
| TCTTCTAAGT CCTCTTCCAG CCTCACTTTG AGTCCTCCTT GGGGGTTGAT AGGAANTNTC | 360 |
| TCTTGGCTTT CTCAATAAAA TCTCTATCCA TCTCATGTTT AATTGGTAC GCNTAAAAAT | 420 |
| GCTGAAAAAA TTAAAATGTT CTGGTTTNCN TTTAAAAAAA AAAAAAAA AAAAAAA | 476 |

(2) INFORMATION FOR SEQ ID NO:81:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 232 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:81:

| | |
|---|-----|
| TTTTTTTTTG TATGCCNTCN CTGTGGNGTT ATTGTTGCTG CCACCCCTGGA GGAGCCCCAGT | 60 |
| TTCTCTGTA TCTTTCTTTT CTGGGGATC TTCCTGGCTC TGCCCCCTCCA TTCCCAGCCT | 120 |
| CTCATCCCCA TCTTGCACTT TTGCTAGGGT TGGAGGGCCT TTCCTGGTAG CCCCTCAGAG | 180 |
| ACTCAGTCAG CGGGATAAAG TCCTAGGGT GGGGGGTGTG GCAAGCCGGC CT | 232 |

(2) INFORMATION FOR SEQ ID NO:82:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 383 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:82:

| | | | |
|------------------------|------------------------|-----------------------|-----|
| AGGCGGGAGC AGAACGCTAAA | GCCAAAGCCC AAGAACAGTG | GCAGTGCCAG CACTGGTGCC | 60 |
| AGTACCAAGTA CCAATAACAT | GCCAGTGCCA GTGCCAGCAC | CAGTGGTGGC TTCAGTGCTG | 120 |
| GTGCCAGCCT GACGCCACT | CTCACATTG GGCTCTTCGC | TGGCCTTGGT GGAGCTGGTG | 180 |
| CCAGCACCAAG TGGCAGCTCT | GGTGCCTGTG GTTTCCTCCTA | CAAGTGAGAT TTTAGATATT | 240 |
| GTAAATCCTG CCAGTCTTC | TCTTCAAGCC AGGGTGCATC | CTCAGAAACC TACTCAACAC | 300 |
| AGCACTCTNG GCAGCCACTA | TCAATCAATT GAAGTTGACA | CTCTGCATTA AATCTATTG | 360 |
| CCATTCAAA | AAAAAAAAAA AAA | | 383 |

(2) INFORMATION FOR SEQ ID NO:83:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 494 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:83:

| | |
|---|-----|
| ACCGAATTGG GACCGCTGGC TTATAAGCGA TCATGTCTC CAGTATTACC TCAACGAGCA | 60 |
| GGGAGATCGA GTCTATACGC TGAAGAAAATT TGACCCGATG GGACAAACAGA CCTGCTCAGC | 120 |
| CCATCCTGCT CGGTTCTCCC CAGATGACAA ATACTCTCGA CACCGAATCA CCATCAAGAA | 180 |
| ACGCTTCAAG GTGCTCATGA CCCAGCAACC GCGCCTGTC CTCTGAGGGT CCTTAAACTG | 240 |
| ATGTCTTTTC TGCCACCTGT TACCCCTCGG AGACTCCGTA ACCAAACTCT TC GGACTGTG | 300 |
| AGCCCTGATC CCTTTTGC AGCCATACTC TTGGCNTCC AGTCTCTCGT GGC GATTGAT | 360 |
| TATGCTTGTG TGAGGCAATC ATGGTGGCAT CACCCATNAA GGGAACACAT TTGANTTTT | 420 |
| TTTCNCATAT TTAAATTAC NACCGAATA NTTCAGAATA AATGAATTGA AAAACTCTTA | 480 |
| AAAAAAAAAA AAAA | 494 |

(2) INFORMATION FOR SEQ ID NO:84:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 380 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:84:

| | |
|--|-----|
| GCTGGTAGCC TATGGCGTGG CCACGGANGG GCTCCTGAGG CACGGGACAG TGACTTCCA | 60 |
| AGTATCCTGC GCCCGTCTT CTACCGTCCC TACCTGCAGA TCTTCGGCA GATTCCCCAG | 120 |
| GAGGACATGG ACCTGGCCCT CATGGACAC AGCAACTGCT CGTCGGAGCC CGGCTTCTGG | 180 |
| GCACACCCCTC CTGGGGCCA GGCGGGCACC TGCGTCTCCC AGTATGCCAA CTGGCTGGTG | 240 |
| GTGCTGCTCC TCGTCATCTT CCTGCTCGTG GCCAACATCC TGCTGGCAC TTGCTCATTG | 300 |
| CCATGTTCAAG TTACACATTC GGCAAAGTAC AGGGCAACAG CNATCTCTAC TGGGAAGGCC | 360 |
| AGCGTTNCCG CCTCATCCGG | 380 |

(2) INFORMATION FOR SEQ ID NO:85:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 481 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:85:

| | | | |
|------------------------|-------------------------|-----------------------|-----|
| GAGITAGCTC CTCCACAACC | TTGATGAGGT CGTCTGCAGT | GGCCTCTCGC TTCATACCGC | 60 |
| TNCCATCGTC ATACTGAGG | TTGCCACCA CCTCCTGCAT | CTTGGGGCGG CTAATATCCA | 120 |
| GGAAACTCTC ATCAAGTCA | CCGTCNATNA AACCTGTGGC | TGGTTCTGTC TTCCGCTCGG | 180 |
| TGTGAAAGGA TCTCCAGAG | GAGTGCTCGA TCTTCCCCAC | ACTTTGATG ACTTTATTGA | 240 |
| GTCGATTCTG CATGTCAGC | AGGAGGTTGT ACCAGCTCTC | TGACAGTGAG GTCACCAGCC | 300 |
| CTATCATGCC NTTAACGTC | CCGAAAGAACAA CCGAGCCTTG | TGTGGGGGGT GNAGTCTCAC | 360 |
| CCAGATTCTG CATTACAGA | NAGCCGTGGC AAAAGANATT | GACAACTCGC CCAGGNNGAA | 420 |
| AAAAGAACACC TCCTGGAAGT | GCTNGCCGCT CCTCGCCNT | TGGTGGNNNGC GCNTNCCTT | 480 |
| T | | | 481 |

(2) INFORMATION FOR SEQ ID NO:86:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 472 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:86:

| | | | |
|-----------------------|------------------------|------------------------|-----|
| AACATCTTCC TGTATAATGC | TGTGTAATAT CGATCCGATN | TTGCTGCTG AGAATTCA | 60 |
| ACTTGGAAAA GCAACTTNAA | GCCTGGACAC TGGTATTAAA | ATTCAACAATA TGCAACACTT | 120 |
| TAAACAGTGT GTCAATCTGC | TCCCCTTACTT TGTCATCACC | AGTCTGGAA TAAGGGTATG | 180 |
| CCCTATTCAAC | ACCTGTTAAAGGGCGCTAA | GCATTTTGA TTCAACATCT | 240 |
| CACAAAGTCG | AAAAAGCAA AAGTAAACAG | TTNTTAATTG GTTAGCCAAT | 300 |
| CATGGACAG AGCCATTGAA | TTTAAAAAGC AAATTGCATA | ATATTGAGCT TTGGGAGCTG | 360 |
| ATATTTGAGC | GGAAAGANTAG CCTTTCTACT | TCACCAAGACA CAACTCCTT | 420 |
| TGTTNACNAA AGTTATGTCT | CTTACAGATG GGATGCTTT | CATATTGGGA TG | 472 |

(2) INFORMATION FOR SEQ ID NO:87:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 413 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:87:

| | |
|--|-----|
| AGAAAACCGT ATCTCTNAAA ACAACCTCTC ATACCTTG TG GACCTAATTT TGTGTGCGTG | 60 |
| TGTGTGCGG CGCATATTAT ATAGACAGGC ACATCTTTT TACTTTGTA AAAGCTTATG | 120 |
| CCTCTTGGT ATCTATATCT GTGAAAGTT TAATGATCTG CCATAATGTC TTGGGGACCT | 180 |
| TTGTCTTCTG TGTAAATGGT ACTAGAGAAA ACACCTATNT TATGAGTCAA TCTAGTTNGT | 240 |
| TTTATTGAC ATGAAGGAAA TTTCCAGATN ACAACACTNA CAAACTCTCC CTTGACTAGG | 300 |
| GGGGACAAAG AAAAGCANAA CTGAACATNA GAAACAATTN CCTGGTGAGA AATTNCATAA | 360 |
| ACAGAAAATTG GGTNGTATAT TGAAANANNG CATCATTNAA ACGTTTTTT TTT | 413 |

(2) INFORMATION FOR SEQ ID NO:88:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 448 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:88:

| | |
|---|-----|
| CGCAGCGGGT CCTCTCTATC TAGCTCCAGC CTCTCGCCTG CCCCACCTCCC CGCGTCCCC | 60 |
| GTCCTAGCCN ACCATGGCCG GGCCCCCTGCG CGCCCCGCTG CTCCCTGCTGG CCATCCTGGC | 120 |
| CGTGGCCCTG GCCGTGAGCC CCGCGGCCGG CTCCAGTCCC GGCAAGCCGC CGCGCCTGGT | 180 |
| GGGAGGCCCA TGGACCCCCC GTGGAAGAAG AAGGTGTGCG GCGTGCACTG GACTTTGCCG | 240 |
| TCGGCNANTA CAACAAACCC GCAACNACTT TTACCNAGCN CGCGCTGCAG GTTGTGCCG | 300 |
| CCCAANAAA TTGTTACTNG GGGTAANTAA TTCTTGAAG TTGAACCTGG GCCAAACNNG | 360 |
| TTTACCAAGA CCNAGCCAAT TNGAACAAATT NCCCTCCAT AACAGCCCCCT TTTAAAAAGG | 420 |
| GAANCANTCC TGNTCTTTT CAAATTTC | 448 |

(2) INFORMATION FOR SEQ ID NO:89:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 463 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:89:

| | |
|--|-----|
| GAATTTGTG CACTGGCCAC TGTGATGGAA CCATTGGGCC AGGATGCTTT GAGTTTATCA | 60 |
| GTAGTGATTC TGCCAAAGTT GGTGTTGTA CATGAGTATG TAAAATGTCA AAAAATTAGC | 120 |
| AGAGGTCTAG GTCTGCATAT CAGCAGACAG TTTGTCGGTG TATTTTGATG CCTTGAAAGTT | 180 |
| CTCAGTGACA AGTTNNNTCT GATGCGAAGT TCTNATTCCA GTGTTTTAGT CCTTTGCATC | 240 |
| TTTNATGTTN AGACTTGCT CTNTNAAATT GCTTTGTNT TCTGCAAGTA CTATCTGTGG | 300 |
| TTAACAAAA TAGAANNACT TCTCTGCTTN GAANATTGA ATATCTTACA TCTNAAAATN | 360 |
| AATTCTCTCC CCATANNAAA ACCCANGCCC TTGGGANAAT TTGAAAAANG GNTCCTTCNN | 420 |
| AATTCCNNANA ANTCAGNTN TCATACAAACA NAACNGGANC CCC | 463 |

(2) INFORMATION FOR SEQ ID NO:90:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:90:

| | | | | | | |
|------------|------------|------------|-------------|------------|------------|-----|
| AGGGATTGAA | GGTCTNTNT | ACTGTGGAC | TGTTCANCCA | CCAACTCTAC | AAGTTGCTGT | 60 |
| CTTCCACTCA | CTGTCTGTA | GCNTNTAAC | CCAGACTGTA | TCTTCATAAA | TAGAACAAAT | 120 |
| TCTTCAACAG | TCACATCTTC | TAGGACCTTT | TTGGATTCAAG | TTAGTATAAG | CTCTTCCACT | 180 |
| TCTCTTGTTA | AGACTTCATC | TGGTAAAGTC | TTAAGTTTG | TAGAAAGGAA | TTAAATTGCT | 240 |
| CGTTCTCTAA | CAATGTCCTC | TCCTTGAAGT | ATTTGGCTGA | ACAACCCACC | TNAAGTCCCT | 300 |
| TTGTGCATCC | ATTTAAATA | TACTTAATAG | GGCATGGTN | CACTAGGTTA | AATTCTGCAA | 360 |
| GAGTCATCTG | TCTGCAAAAG | TTGCGTTAGT | ATATCTGCCA | | | 400 |

(2) INFORMATION FOR SEQ ID NO:91:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 480 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:91:

| | | | | | | |
|-------------|------------|------------|------------|------------|------------|-----|
| GAGCTCGGAT | CCAATAATCT | TTGTCTGAGG | GCAGCACACA | TATNCAGTGC | CATGGNAACT | 60 |
| GGTCTACCCC | ACATGGGAGC | AGCATGCCGT | AGNTATATAA | GGTCATTCCC | TGAGTCAGAC | 120 |
| ATGCCCTTT | GACTACCGTG | TGCCAGTGC | GGTGATTCTC | ACACACCTCC | NNCCGCTCTT | 180 |
| TGTGGAAAAAA | CTGGCACTTG | NCTGGAACTA | GCAAGACATC | ACTTACAAAT | TCACCCACGA | 240 |
| GACACTTGAA | AGGTGTAACA | AAGCGACTCT | TGCATTGCTT | TTTGTCCCTC | CGGCACCAGT | 300 |
| TGTCAATACT | AACCCGCTGG | TTTGCCTCCA | TCACATTGT | GATCTGTAGC | TCTGGATACA | 360 |
| TCTCTGACA | GTACTGAAGA | ACTTCTTCTT | TTGTTTCAA | AGCAACTCTT | GGTGCCTGTT | 420 |
| NGATCAGGTT | CCCATTTCCC | AGTCCGAATG | TTCACATGGC | ATATNTTACT | TCCCACAAAA | 480 |

(2) INFORMATION FOR SEQ ID NO:92:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 477 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:92:

| | |
|---|-----|
| ATACAGCCA NATCCCACCA CGAAGATGCG CTTGTTGACT GAGAACCTGA TGGGGTCACT | 60 |
| GGTCCCCCTG TAGCCCCAGC GACTCTCCAC CTGCTGGAAG CGGTTGATGC TGCACTCCTT | 120 |
| CCCACGCAGG CAGCAGCGGG GCCGGTCAAT GAACTCCACT CGTGGCTTGG GTTGACGGT | 180 |
| TAANTGCAGG AAGAGGCTGA CCACCTCGCG GTCCACCAGG ATGCCCGACT GTGCGGGACC | 240 |
| TGCAAGCGAAA CTCCTCGATG GTCATGAGCG GGAAGCGAAT GANGCCCAGG GCCTTGCCCCA | 300 |
| GAACCTTCCG CCTGTTCTCT GGCCTCACCT GCAGCTGCTG CCGCTNACAC TCGGCCTCGG | 360 |
| ACCAGCGGAC AAACGGCGTT GAACAGCGC ACCTCACCGA TGCCCANTGT GTCGCGCTCC | 420 |
| AGGAACGGCN CCAGCGTGTC CAGGTCAATG TCGGTGAANC CTCCGCGGGT AATGGCG | 477 |

(2) INFORMATION FOR SEQ ID NO:93:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 377 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:93:

| | |
|--|-----|
| GAACGGCTGG ACCTTGCCTC GCATTGTGCT GCTGGCAGGA ATACCTTGGC AAGCAGCTCC | 60 |
| AGTCCGAGCA GCCCCAGACC GCTGCCGCCC GAAGCTAAGC CTGCCTCTGG CCTTCCCCCTC | 120 |
| CGCCCTCAATG CAGAACCCANT AGTGGGAGCA CTGTTTTAG AGTTAAGAGT GAACACTGTN | 180 |
| TGATTTACT TGGGAAATTTC CTCTGTATA TAGTTTTCC CAATGCTAAT TTCCAAACAA | 240 |
| CAACAACAAA ATAACATGTT TGCCCTTNA GTTGATAAA AGTANGTGTAT TCTGTATNTA | 300 |
| AAGAAAATAT TACTGTTACA TATACTGCTT GCAANTTCTG TATTTATTGG TNCTCTGGAA | 360 |
| ATAAAATATAT TATTAAGA | 377 |

(2) INFORMATION FOR SEQ ID NO:94:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 495 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:94:

| | |
|---|-----|
| CCCTTTGAGG GGTTAGGGTC CAGTCCCAG TGGAAAGAAC AGGCCAGGAG AANTGCGTGC | 60 |
| CGAGCTGANG CAGATTTCCC ACAGTGACCC CAGAGCCCTG GGCTATAGTC TCTGACCCCT | 120 |
| CCAAGGAAAG ACCACCTTCT GGGGACATGG GCTGGAGGGC AGGACCTAGA GGCACCAAGG | 180 |
| GAAGGGCCCA TTCCGGGGCT GTTCCCCGAG GAGGAAGGGGA AGGGGCTCTG TGTGCCCCC | 240 |
| ACGAGGAANA GGCCCTGANT CCTGGGATCA NACACCCCTT CACGTGTATC CCCACACAAA | 300 |
| TGCAAGCTCA CCAAGGTCCC CTCTCAGTCC CTTCCCTACA CCCTGAACGG NCACGGCCC | 360 |
| ACACCCACCC AGANCANCCA CCCGCCATGG GGAATGTNCT CAAGGAATCG CNGGGCAACG | 420 |
| TGGACTCTNG TCCCNNAAGG GGGCAGAATC TCCAATAGAN GGANNGAAC CTTGCTNANA | 480 |
| AAAAAAAANA AAAAAA | 495 |

(2) INFORMATION FOR SEQ ID NO:95:

- (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 472 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:95:

| | | | | | | |
|-------------|------------|------------|------------|------------|------------|-----|
| GGTTACTTGG | TTTCATTGCC | ACCACTTAGT | GGATGTCATT | TAGAACATT | TTGTCTGCTC | 60 |
| CCTCTGGAAG | CCTTGCGCAG | AGCGGACTTT | GTAATTGTTG | GAGAATAACT | GCTGAATT | 120 |
| TAGCTGTTT | GAGTTGATTG | GCACCACTC | ACCAACTC | AATATGAAA | CTATTTNACT | 180 |
| TATTTTATTAT | CTTGTGAAAA | GTATACAATG | AAAATTGTTG | TCATACTGTA | TTTATCAAGT | 240 |
| ATGATGAAAA | GCAATAGATA | TATATTCTT | TATTATGTTN | AATTATGATT | GCCATTATTA | 300 |
| ATCGGCAAAA | TGTGGAGTGT | ATGTTCTTT | CACAGTAATA | TATGCCCTTT | GTAACATTAC | 360 |
| TTGGTTATT | TATTGTAAT | GAATTACAAA | ATTCTTAATT | TAAGAAAATG | GTANGTTATA | 420 |
| TTTANTTCAN | TAATTTCTT | CCTTGTAC | GTTAATTG | AAAAGAATGC | AT | 472 |

(2) INFORMATION FOR SEQ ID NO:96:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 476 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:96:

| | | | | | | |
|------------|------------|------------|------------|------------|------------|-----|
| CTGAAGCATT | TCTTCAAAC | TNTCTACTTT | TGTCATTGAT | ACCTGTAGTA | AGTTGACAAT | 60 |
| GTGGTGAAAT | TTCAAAATTA | TATGTAAC | CTACTAGTTT | TACTTTCTCC | CCCAAGTCTT | 120 |
| TTTTAACTCA | TGATTTTAC | ACACACAATC | CAGAACTTAT | TATATAGCCT | CTAAAGTCTT | 180 |
| ATTCTTCACA | GTAGATGATG | AAAGAGTCCT | CCAGTGTCTT | GNGCANAATG | TTCTAGNTAT | 240 |
| AGCTGGATAC | ATACNGTGGG | AGTTCTATAA | ACTCATACCT | CAGTGGGACT | NAACCAAAT | 300 |
| TGTGTTAGTC | TCAATTCTA | CCACACTGAG | GGAGCCTCCC | AAATCACTAT | ATTCTTATCT | 360 |
| GCAGGTACTC | CTCCAGAAA | ACNGACAGGG | CAGGCTTGCA | TGAAAAGTN | ACATCTGCGT | 420 |
| TACAAAGTCT | ATCTTCCTCA | NANGTGTN | AAGGAACAAT | TTAATCTTCT | AGCTTT | 476 |

(2) INFORMATION FOR SEQ ID NO:97:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 479 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:97:

| | | | | | | |
|------------|------------|------------|------------|------------|------------|----|
| ACTCTTTCTA | ATGCTGATAT | GATCTTGAGT | ATAAGAATGC | ATATGTCACT | AGAATGGATA | 60 |
|------------|------------|------------|------------|------------|------------|----|

| | |
|---|-----|
| AAATAATGCT GCAAACCTAA TGTCTTATG CAAAATGGAA CGCTAATGAA ACACAGCTTA | 120 |
| CAATCGCAA TCAAAACTCA CAAGTCCTCA TCTGTGTAG ATTTAGTGTAA ATAAGACTTA | 180 |
| GATTGTGCTC CTTCGGATAT GATTGTTCT CANATCTTGG GCAATNTTCC TTAGTCAAAT | 240 |
| CAAGCTACTA GAATTCTGTT ATTGGATATN TGAGAGCATG AAATTTTAA NAATACACTT | 300 |
| GTGATTATNA AATTAATCAC AAATTTCACT TATACCTGCT ATCAGCAGCT AGAAAAACAT | 360 |
| NTNNNTTTA NATCAAAGTA TTTTGTGTTT GGAANTGTNN AAATGAAATC TGAATGTGGG | 420 |
| TTCNATCTTA TTTTTCCCN GACNACTANT TNCTTTTTA GGGNCTATTG TGANCCATC | 479 |

(2) INFORMATION FOR SEQ ID NO:98:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 461 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:98:

| | |
|---|-----|
| AGTGACTTGT CCTCCAACAA AACCCCTTGA TCAAGTTGT GGCACTGACA ATCAGACCTA | 60 |
| TGCTAGTTCC TGTCACTAT TCGCTACTAA ATGCAGACTG GAGGGGACCA AAAAGGGGCA | 120 |
| TCAACTCCAG CTGGATTATT TTGGAGCTG CAAATCTATT CCTACTTGTAA CGGACTTTGA | 180 |
| AGTGATTCTAG TTTCCCTCAC GGATGAGAGA CTGGCTCAAG AATATCCTCA TGCACTTTA | 240 |
| TGAAGCCACT CTGAACACGC TGTTATCTA GTGAGAAACA GAGAAATAAA GTCAAGAAAT | 300 |
| TTACCTGGAG AAAAGAGGCT TTGGCTGGGG ACCATCCCCT TGAACCTTCT CTTAAGGACT | 360 |
| TTAAGAAAAA CTACCACATG TTGTGTATCC TGGTGCCTGG CGTTTATGAA CTGACCACCC | 420 |
| TTTGAATAA TCTTGACGCT CCTGAACCTG CTCCTCTGCG A | 461 |

(2) INFORMATION FOR SEQ ID NO:99:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 171 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:99:

| | |
|--|-----|
| GTGGCCGCGC GCAGGTGTTT CCTCGTACCG CAGGGCCCC TCCCTTCCCC AGGCGTCCCT | 60 |
| CGGCGCCTCT CGGGGGCCGA GGAGGAGCGG CTGGCGGGTG GGGGGAGTGT GACCCACCC | 120 |
| CGGTGAGAAA AGCCTTCTCT AGCGATCTGA GAGGCCTGCC TTGGGGTAC C | 171 |

(2) INFORMATION FOR SEQ ID NO:100:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 269 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:100:

| | | | | | | |
|------------|------------|------------|------------|------------|------------|-----|
| CGGCCGCAAG | TGCAACTCCA | GCTGGGGCCG | TGCGGACGAA | GATTCTGCCA | GCACTTGGTC | 60 |
| CGACTGCGAC | GACGGCGGC | GCGACAGTCG | CAGGTGCAGC | GCGGGCGCCT | GGGGTCTTGC | 120 |
| AAGGCTGAGC | TGACGCCGCA | GAGGTCGTGT | CACGTCCCAC | GACCTTGACG | CCGTCGGGA | 180 |
| CAGCCGGAAC | AGAGCCCGGT | GAAGCGGGAG | GCCTCGGGGA | GCCCCTCGGG | AAGGGCGGCC | 240 |
| CGAGAGATAC | GCAGGTGCAG | GTGGCCGCC | | | | 269 |

(2) INFORMATION FOR SEQ ID NO:101:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 405 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:101:

| | | | | | | |
|-------------|------------|------------|------------|------------|------------|-----|
| TTTTTTTTTT | TTTTGGAATC | TACTGCGAGC | ACAGCAGGTC | AGCAACAAGT | TTATTTTGCA | 60 |
| GCTAGCAAGG | TAACAGGGTA | GGGCATGGTT | ACATGTTAG | GTCAACTTCC | TTTGTCTGG | 120 |
| TTGATTTGGTT | TGTCTTTATG | GGGGCGGGGT | GGGGTAGGGG | AAACGAAGCA | AATAACATGG | 180 |
| AGTGGGTGCA | CCCTCCCTGT | AGAACCTGGT | TACAAAGCTT | GGGGCAGTTC | ACCTGGTCTG | 240 |
| TGACCGTCAT | TTCTTGACA | TCAATGTTAT | TAGAAGTCAG | GATATCTTTT | AGAGAGTCCA | 300 |
| CTGTTCTGGA | GGGAGATTAG | GGTTTCTTGC | CAAATCCAAC | AAAATCCACT | GAAAAAGTTG | 360 |
| GATGATCAGT | ACGAATACCG | AGGCATATTG | TCATATCGGT | GGCCA | | 405 |

(2) INFORMATION FOR SEQ ID NO:102:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 470 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:102:

| | | | | | | |
|------------|------------|------------|------------|-------------|------------|-----|
| TTTTTTTTTT | TTTTTTTTTT | TTTTTTTTTT | TTTTTTTTTT | TTTTTTTTTT | TTTTTTTTTT | 60 |
| GSCACTTAAT | CCATTTTAT | TCAAAATGT | CTACAAATT | AATCCCATT | TACGGTATT | 120 |
| TCAAAATCTA | AATTATTCAA | ATTAGCCAA | TCCTTACCAA | ATAATACCCA | AAAATCAAAA | 180 |
| ATATACTTCT | TTCAGCAAAC | TTGTTACATA | AATTAACAAA | ATATATAACGG | CTGGTGT | 240 |
| CAAAGTACAA | TTATCTTAAC | ACTGCAAACA | TTTAAGGAA | CTAAAATAAA | AAAAAACACT | 300 |
| CCGCAAAGGT | TAAGGGAAC | AACAAATTCT | TTTACAACAC | CATTATAAAA | ATCATATCTC | 360 |
| AAATCTTAGG | GGAATATATA | CTTCACACGG | GATCTTAAC | TTTACTCACT | TTGTTATTT | 420 |
| TTTAAACCA | TTGTTGGGC | CCAACACAAT | GGAATCCCC | CTGGACTAGT | | 470 |

(2) INFORMATION FOR SEQ ID NO:103:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 581 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:103:

| | | | | | | |
|------------|------------|------------|------------|------------|-------------|-----|
| TTTTTTTTT | TTTTTTTG | CCCCCTCTT | ATAAAAAAC | AGTACCAATT | TTATTTTACT | 60 |
| TACACATATT | TATTTTATAA | TTGGTATTAG | ATATTCAAA | GGCAGCTTT | AAAATCAAAC | 120 |
| TAATGGAAA | CTGCCTTAGA | TACATAATT | TTAGGAATT | GCTAAAATC | TGCCTAAAGT | 180 |
| GAAAATCTTC | TCTAGCTTT | TTGACTGTAA | ATTTTGACT | CTTGTAAC | ATCCAAATT | 240 |
| ATTTTCTTG | TCTTTAAAAT | TATCTAATCT | TTCCATTTT | TCCCTATTCC | AAGTCAATT | 300 |
| GCTTCTCTAG | CCTCATTTCC | TAGCTTTAT | CTACTATTAG | TAAGTGGTT | TTTCCTAA | 360 |
| AGGGAAAACA | GGAAGAGAAA | TGGCACACAA | AACAAACATT | TTATATT | CAT ATTACCT | 420 |
| ACGTTAATAA | ATAGCATT | TGTGAAGCCA | GCTAAAAGA | AGGCTTAGAT | CCTTITATGT | 480 |
| CCATTTAGT | CACTAAACGA | TATCAAAGTG | CCAGAATGCA | AAAGGTTGT | GAACATT | 540 |
| TCAAAAGCTA | ATATAAGATA | TTTCACATAC | TCATCTTCT | G | | 581 |

(2) INFORMATION FOR SEQ ID NO:104:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 578 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:104:

| | | | | | |
|------------|-------------|-----------|-------------|------------|-----|
| TTTTTTTTT | TTTTTCTCTT | CTTTTTTTT | GAAATGAGGA | TCGAGTTTT | 60 |
| CACTCTCTAG | ATAGGGCATG | AAGAAAAC | TC ATCTCCAG | CTTAA | 120 |
| CTCTTATGCT | ATATCATATT | TTAAGTAA | CTAATGAGTC | ACTGGCTT | 180 |
| AGGAAATCTG | TTCATTCCTTC | TCATTCAT | AGTATATCA | AGTACTAC | 240 |
| GAGGTTTTTC | TTCTCTATT | ACATCTATT | TTCCATGTGA | ATTGTATCA | 300 |
| TTCATGCAA | CTAGAAAATA | ATGTTCTT | TGCATAAGAG | AAGAGAACAA | 360 |
| CAAAACTGCT | CAAATTGTT | GTAAAGTT | CCATTATAAT | TAGTTGCCAG | 420 |
| AAATCACATT | TACGACAGCA | ATAATAAAC | TGAAGTACCA | GTAAATATC | 480 |
| AAAGGAACAT | TTTTAGCCTG | GGTATAATT | GCTAATT | CAAGCA | 540 |
| TGAATT | CACA | TGTTATT | CCTAGCCC | ACAAATGG | 576 |

(2) INFORMATION FOR SEQ ID NO:105:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 538 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:105:

| | |
|---|-----|
| TTTTTTTTTT TTTTCAGTA ATAATCAGAA CAATATTAT TTTTATATT AAAATTCTATA | 60 |
| GAAAAGTGC TTACATTTAA TAAAAGTTG TTTCTCAAAG TGATCAGAGG AATTAGATAT | 120 |
| GTCTTGAAACA CCAATATTAA TTTGAGGAAA ATACACCAAA ATACATTAAG TAAATTATT | 180 |
| AAGATCATAG AGCTTGTAA TGAAAAGATA AAATTGACC TCAGAAACTC TGAGCATTAA | 240 |
| AAATCCACTA TTAGCAAATA AATTACTATG GACTTCTTGC TTTAATTTG TGATGAATAT | 300 |
| GGGGTGTAC TGGTAAACCA ACACATTCTG AAGGATACAT TACTTAGTGA TAGATTCTTA | 360 |
| TGTACTTTGC TAATACGTGG ATATGAGTTG ACAAGTTCT CTTTCTCAA TCTTTAAGG | 420 |
| GGCGAGAAAT GAGGAAGAAA AGAAAAGGAT TACGCATACT GTTCTTCTA TGGAACGATT | 480 |
| AGATATGTTT CCTTGCCTA TATTAACAAA ATAATAATGT TTACTACTAG TGAAACCC | 538 |

(2) INFORMATION FOR SEQ ID NO:106:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 473 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:106:

| | |
|--|-----|
| TTTTTTTTTT TTTTTTAGTC AAGTTTCTAT TTTTATTATA ATTAAAGTCT TGGTCATTTC | 60 |
| ATTATTTAGC TCTGCACTT ACATATTAA ATTAAAGAAA CGTTTTAGAC AACTGTACAA | 120 |
| TTTATAATG TAAGGTGCCA TTATTGAGTA ATATATTCCCT CCAAGAGTGG ATGTGTCCCT | 180 |
| TCTCCCACCA ACTAATGAAC AGAACACATTA GTTTAATTTT ATTAGTAGAT ATACACTGCT | 240 |
| GCAAACGCTA ATTCTCTTCT CCATCCCCAT GTGATATTGT GSTATATGTGT GAGTTGGTAG | 300 |
| AATGCATCAC AATCTACAAAT CAACAGCAAG ATGAAGCTAG GCTGGGCTTT CGGTGAAAAT | 360 |
| AGACTGTGTC TGTCTGAATC AAATGATCTG ACCTATCCTC GGTGGCAAGA ACTCTTCGAA | 420 |
| CCGCTTCCTC AAAGGCGCTG CCACATTGT GGCTCTTGC ACTTGTTCGA AAA | 473 |

(2) INFORMATION FOR SEQ ID NO:107:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1621 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:107:

| | |
|--|-----|
| CGCCATGGCA CTGCAGGGCA TCTCGGTATG GGAGCTGTCC GGCCTGGCCC CGGGCCCGTT | 60 |
| CTGTGCTATG GTCCTGGCTG ACTTCGGGGC GCGTGTGGTA CGCGTGGACC GGCCCGGCTC | 120 |
| CCGCTACGAC GTGAGCCGCT TGGGCCGGG CAAGCGCTCG CTAGTGTCTGG ACCTGAAGCA | 180 |
| GCCGCGGGGA GCGCCGTGC TGCGCGTCT GTGCAAGCGG TCGGATGTGC TGCTGGAGCC | 240 |
| CTTCCGCCGC GGTGTATGG AGAAACCTCA GCTGGGCCA GAGATTCTGC AGCGGGAAAA | 300 |
| TCCAAGGCTT ATTTATGCA GGCTGAGTGG ATTGGCCAG TCAGGAAGCT TCTGCCGGTT | 360 |
| AGCTGGCCAC GATATCAACT ATTTGGCTTT GTCAAGGTGT CTCTCAAAAAA TTGGCAGAAG | 420 |
| TGGTGAGAAT CGCTATGCC CGCTGAATCT CCTGGCTGAC TTTGCTGGTG GTGGCCTTAT | 480 |
| GTGTGCACTG GGCATTATAA TGCGCTTT TGACCGCACA CGCAGTACAGA AGGGTCAGGT | 540 |

| | |
|--|------|
| CATTGATGCA AATATGGTGG AAGGAACAGC ATATTTAAGT TCTTTCTGT GGAAAACCTCA | 600 |
| GAATCGAGT CTGTGGGAAG CACCTCGAGG ACAGAACATG TTGGATGGTG GAGCACCTT | 660 |
| CTATACGACT TACAGGACAG CAGATGGGA ATTCACTGGCT GTGGAGCAA TAGAACCCCA | 720 |
| GTTCTACGAG CTGCTGATCA AAGGACTTGG ACTAAAGTCT GATGAACCTTC CCAATCAGAT | 780 |
| GAGCATGGAT GATTGGCCAG AAATGAAGAA GAAGTTGCA GATGTATTG CAAAGAAGAC | 840 |
| GAAGGCAGAG TGGTGTCAAA TCTTGACGG CACAGATGCC TGTGTGACTC CGGTTCTGAC | 900 |
| TTTGAGGAG GTTGTTCATC ATGATCACAA CAAGGAACGG GGCTCGTTTA TCACCAGTGA | 960 |
| GGAGCAGGAC GTGAGCCCC GCCCCTGCACC TCTGCTGTTA AACACCCCCAG CCATCCCTTC | 1020 |
| TTTCAAAAGG GATCCTTTCA TAGGAGAACAA CACTGAGGAG ATACTTGAAAG AATTGGATT | 1080 |
| CAGCCGCGAA GAGATTTATC AGCTTAACTC AGATAAAATC ATTGAAAGTA ATAAGGTAAA | 1140 |
| AGCTAGTC TAACTTCCAG GCCCACGGCT CAAGTGAATT TGAATACGTG ATTTACAGTG | 1200 |
| TAGAGTAACA CATAACATTG TATGCATGGA AACATGGAGG AACAGTATTA CAGTGTCCCTA | 1260 |
| CCACTCTAAAT CAAGAAAAGA ATTACAGACT CTGATTCTAC AGTGATGATT GAATTCTAAA | 1320 |
| AATGGTTATC ATTAGGGCTT TTGATTTGGG TACTTATACT AAATTATGGT | 1380 |
| AGTATTCTG CCTTCCAGTT TGCTTGATAT ATTTGTTGAT ATTAAAGATTC TTGACTTATA | 1440 |
| TTTGAATGG GTTCTAGTG AAAAGGAATG ATATATTCTT GAAGACATCG ATATACATT | 1500 |
| ATTACACTC TTGATTCTAC AATGTAGAAA ATGAGGAAAT GCCACAAATT GTATGGTGAT | 1560 |
| AAAAGTCACG TGAAACAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA | 1620 |
| A | 1621 |

(2) INFORMATION FOR SEQ ID NO:108:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 382 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:108:

| | | | |
|---|-----|-----|-----|
| Met Ala Leu Gln Gly Ile Ser Val Met Glu Leu Ser Gly Leu Ala Pro | | | |
| 1 | 5 | 10 | 15 |
| Gly Pro Phe Cys Ala Met Val Leu Ala Asp Phe Gly Ala Arg Val Val | | | |
| 20 | 25 | 30 | |
| Arg Val Asp Arg Pro Gly Ser Arg Tyr Asp Val Ser Arg Leu Gly Arg | | | |
| 35 | 40 | 45 | |
| Gly Lys Arg Ser Leu Val Leu Asp Leu Lys Gln Pro Arg Gly Ala Ala | | | |
| 50 | 55 | 60 | |
| Val Leu Arg Arg Leu Cys Lys Arg Ser Asp Val Leu Leu Glu Pro Phe | | | |
| 65 | 70 | 75 | 80 |
| Arg Arg Gly Val Met Glu Lys Leu Gln Leu Gly Pro Glu Ile Leu Gln | | | |
| 85 | 90 | 95 | |
| Arg Glu Asn Pro Arg Leu Ile Tyr Ala Arg Leu Ser Gly Phe Gly Gln | | | |
| 100 | 105 | 110 | |
| Ser Gly Ser Phe Cys Arg Leu Ala Gly His Asp Ile Asn Tyr Leu Ala | | | |
| 115 | 120 | 125 | |
| Leu Ser Gly Val Leu Ser Lys Ile Gly Arg Ser Gly Glu Asn Pro Tyr | | | |
| 130 | 135 | 140 | |
| Ala Pro Leu Asn Leu Leu Ala Asp Phe Ala Gly Gly Leu Met Cys | | | |
| 145 | 150 | 155 | 160 |
| Ala Leu Gly Ile Ile Met Ala Leu Phe Asp Arg Thr Arg Thr Asp Lys | | | |
| 165 | 170 | 175 | |
| Gly Gln Val Ile Asp Ala Asn Met Val Glu Gly Thr Ala Tyr Leu Ser | | | |
| 180 | 185 | 190 | |
| Ser Phe Leu Trp Lys Thr Gln Lys Ser Ser Leu Trp Glu Ala Pro Arg | | | |
| 195 | 200 | 205 | |

Gly Gln Asn Met Leu Asp Gly Gly Ala Pro Phe Tyr Thr Thr Tyr Arg
 210 215 220
 Thr Ala Asp Gly Glu Phe Met Ala Val Gly Ala Ile Glu Pro Gin Phe
 225 230 235 240
 Tyr Glu Leu Leu Ile Lys Gly Leu Gly Leu Lys Ser Asp Glu Leu Pro
 245 250 255
 Asn Gln Met Ser Met Asp Asp Trp Pro Glu Met Lys Lys Lys Phe Ala
 260 265 270
 Asp Val Phe Ala Lys Lys Thr Lys Ala Glu Trp Cys Gln Ile Phe Asp
 275 280 285
 Gly Thr Asp Ala Cys Val Thr Pro Val Leu Thr Phe Glu Glu Val Val
 290 295 300
 His His Asp His Asn Lys Glu Arg Gly Ser Phe Ile Thr Ser Glu Glu
 305 310 315 320
 Gln Asp Val Ser Pro Arg Pro Ala Pro Leu Leu Leu Asn Thr Pro Ala
 325 330 335
 Ile Pro Ser Phe Lys Arg Asp Pro Phe Ile Gly Glu His Thr Glu Glu
 340 345 350
 Ile Leu Glu Glu Phe Gly Phe Ser Arg Glu Glu Ile Tyr Gln Leu Asn
 355 360 365
 Ser Asp Lys Ile Ile Glu Ser Asn Lys Val Lys Ala Ser Leu
 370 375 380

(2) INFORMATION FOR SEQ ID NO:109:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1524 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:109:

| | | | | | | |
|-------------|------------|-------------|-------------|-------------|------------|------|
| GGCACGAGGC | TGGGCCAGGG | CCTGAGCGGA | GGCGGGGGCA | GCCTGCCAG | CGGGGGCCCC | 60 |
| GGGCTGGCC | ATGCCCTACT | GAGCCAGCGC | CTGCGCTCT | ACCTGCCGA | CAGCTGGAAC | 120 |
| CAGTGCACC | TAGTGGCTCT | CACCTGCTTC | CTCCTGGCG | TGGCTGCCG | GCTGACCCCG | 180 |
| GGTTGTACC | ACCTGGCCG | CACTGTCCTC | TGCATCGACT | TCATGGTTT | CACGGTGCAG | 240 |
| CTGCTTCACA | TCTTCACGGT | CAACAAACAG | CTGGGGCCA | AGATCGTCAT | CGTGAGCAAG | 300 |
| ATGATGAAGG | ACGTGTTCTT | CTTCCTCTTC | TTCTCGGCG | TGTGGCTGGT | AGCCTATGGC | 360 |
| GTGGCCACGG | AGGGGCTCCT | GAGGCCACGG | GACAGTGACT | TCCCAAAGTAT | CCTGCCGCC | 420 |
| GTCTTCTACC | GTCCCTACCT | GCAGATCTC | GGGCAGATT | CCCAGGAGGA | CATGGACGTG | 480 |
| GCCCTCATGG | AGCACAGCAA | CTGCTCGTC | GAGCCGGCT | TCTGGGCACA | CCCTCTGGG | 540 |
| GCCCAGGCGG | GCACCTGCGT | CTCCCACTAT | GCCAACCTGGC | TGGTGGTCT | GCTCCTCGTC | 600 |
| ATCTCTCTGC | TCGTGGCCAA | CATCTGCTG | GTCAACTTGC | TCATTGCCAT | GTTCACTTAC | 660 |
| ACATCGGCA | AAGTACAGGG | CAACAGCGAT | CTCTACTTGA | AGGCGCAGCG | TTACCGCTC | 720 |
| ATCCGGGAAT | TCCACTCTCG | GCCCCGCTG | GCCCCGCCCT | TTATCGTCAT | CTCCCACTTG | 780 |
| CGCTCTCTGC | TCAGGCAATT | GTGCAGGGGA | CCCCGGAGCC | CCAGCGTC | CTCCCCGGCC | 840 |
| CTCGAGCATT | TCCGGGTTTA | CCTTTCTAAG | GAAGCCGAGC | GGAAGCTGCT | AACGTGGAA | 900 |
| TCGGTGCATA | AGGAGAACTT | TCTGCTGGCA | CGCGCTAGGG | ACAAGCGGA | GAGCGACTCC | 960 |
| GAGCGTCTGA | AGCGCACGTC | CCAGAACGGTG | GACTTGGCAC | TGAAACAGCT | GGGACACATC | 1020 |
| CGCGAGTACG | AACAGCGCCT | GAAAGTGTG | GAGCGGGAGG | TCCAGCAGTG | TAGCCCGCTC | 1080 |
| CTGGGGTGGG | TGGCGAGGC | CCTGAGCCGC | TCTGCCCTGC | TGCCCCCAGG | TGGGCCGCCA | 1140 |
| CCCCCTGACC | TGCCCTGGTC | CAAAGACTGA | GCCCTGCTGG | CGGACTTCAA | GGAGAAGCCC | 1200 |
| CCACAGGGGA | TTTTGCTCCT | AGAGTAAGGC | TCATCTGGGC | CTCGGCCCCC | GCACCTGGTG | 1260 |
| GCCTTGTCCCT | TGAGGTGAGC | CCCATGTCCA | TCTGGGCCAC | TGTCAGGACC | ACCTTTGGGA | 1320 |
| GTGTATCCT | TACAAACCAC | AGCATGCCCG | GCTCCTCCCA | GAACCAGTCC | CAGCCTGGGA | 1380 |

| | |
|--|------|
| GGATCAAGGC CTGGATCCCG GGCGTTATC CATCTGGAGG CTGCAGGTC CTTGGGTAA | 1440 |
| CAGGGACAC AGACCCCTCA CCACTCACAG ATTCCCTACA CTGGGAAAT AAAGCCATT | 1500 |
| CAGAGGAAAA AAAAAAAA AAAA | 1524 |

(2) INFORMATION FOR SEQ ID NO:110:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 3410 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:110:

| | |
|---|------|
| GGGAACCAGC CTGCACCGC TGGCTCCGGG TGACAGCCGC GCGCTCGGC CAGGATCTGA | 60 |
| GTGATGAGAC GTGTCCCCAC TGAGGTGCC CACAGCAGCA GGTGGTGGAGC ATGGCCTGAC | 120 |
| AAGCTGGACC GGCAACCAAAG GGCTGGCAGA AATGGGCAGC TGGCTGATTC CTAGGCAGTT | 180 |
| GGCGGCAGCA AGGAGGAGAG GCCGCAGCTT CTGGAGCAGA GCCGAGACGA ACCAGTTCTG | 240 |
| GAGTGCCTGA ACGGCCCTACG GAGCCCTACC CGCCTGGCCC ACTATGGTCC AGAGGCTGTG | 300 |
| GGTGAGCCGC CTGCTGCGGC ACCGGAAAGC CCAGCTCTTG CTGGTCAACC TGCTAACCTT | 360 |
| TGGCTGAGGAG CTGTGTTTGG CCGCAGGCACT CACCTATGTG CCGCCTCTGC TGCTGGAAGT | 420 |
| GGGGTAGAG GAGAAGTCA TGACCATGTT GCTGGCATT GGTCAGTGC TGGGCTGGT | 480 |
| CTGTGTCCTGG CCTCTAGGCT CAGCCAGTGA CCACTGGCGT GGACGCTATG GCCGCCGCCG | 540 |
| GCCCTTCATC TGGGACTGTG CTTGGGCAT CCTGCTGAGC CTCTTCTCA TCCCAAGGGC | 600 |
| CGGCTGGCTA GCAGGGCTGC TGTGCCCGGA TCCCAGGCC CTGGAGCTGG CACTGCTCAT | 660 |
| CCTGGCGTG GGGCTGCTGG ACTTCTGTGG CCAGGTGTGC TTCACTCCAC TGGAGGCCCT | 720 |
| GCTCTCTGAC CTCTCCGGG ACCCGGACCA CTGTCGCCAG GCCTACTCTG TCTATGCCTT | 780 |
| CATGATCAGT CTTGGGGCT GCCTGGCTA CCTCCTGCCT GCCATTGACT GGGACACCAG | 840 |
| TGCCCTGGCC CCCTACCTGG GCACCCAGGA GGAGTGCCTC TTGGCCTGTC TCACCCCTCAT | 900 |
| CTTCCTCACC TGCGTAGCAG CCACACTGCT GGTGGCTGAG GAGGCAAGGC TGGGCCCCAC | 960 |
| CGAGCCAGCA GAAGGGCTGT CGGGCCCTC CTTGTCGCCG CACTGCTGTC CATGCCGGC | 1020 |
| CCGGCTGGCT TTCCGGAAAC TGGGGCGCC GCTTCCCGG CTGCAACCAGC TTGCTGCCG | 1080 |
| CATGCCCGC ACCCTCGGCC GGCTCTCGT GGCTGAGCTG TGCACTGGA TGGCACTCAT | 1140 |
| GACCTTCACG CTGTTTACA CGGATTCCTG GGGCGAGGG CTGTACCAAGG GCGTGCCTCAG | 1200 |
| AGCTGAGCCG GGCACCGAGG CCCGGAGACA CTATGATGAA GGCGTTCGGA TGGCAGCCT | 1260 |
| GGGGCTGTTG CTGAGTGCCTG CCATCTCCCT GGTCTTCTCT CTGGTCATGG ACCGGCTGGT | 1320 |
| GCACCGATTG GGCACTCGAG CAGTCTATTG GGCCAGTGTG GCAGCTTCC CTGTGGCTGC | 1380 |
| CGGTGCCACA TGCTGTCCC ACAGTGTGGC CGTGGTGACA GCTTCAGCG CCCTCACCGG | 1440 |
| GTTCACCTTC TCAGCCCTGC AGATCTGCC CTACACACTG GCCTCCCTCT ACCACCCGGGA | 1500 |
| GAAGCAGGTG TTCTGCCA AATACCGAGG GGACACTGGA GGTGCTAGCA GTGAGGACAG | 1560 |
| CCTGATGACC AGCTCTCTGC CAGGCCCTAA GCCTGGAGCT CCCTCCCTA ATGGACACGT | 1620 |
| GGGTGCTGGA GGCACGGGCC TGCTCCACC TCCACCGCG CCTCTGGGG CCTCTGCCTG | 1680 |
| TGATGTCCTCC GTACGTGTGG TGGTGGTGA GCCACCGAG GCGGGTGG TTCCGGCCCG | 1740 |
| GGGCATCTGC CTGGACCTCG CCATCTGGG TAGTGCCTTC CTGCTGTCCC AGGTGGCCCC | 1800 |
| ATCCCTGTTT ATGGGCTCCA TTGTCCAGCT CAGCCAGTCT GTCACTGCCT ATATGGTGT | 1860 |
| TGCCGCAGGC CTGGGCTGG TCGCCATTAA CTTTGTACA CAGGTAGTAT TTGACAAGAG | 1920 |
| CGACTTGGCC AAATACTCAG CGTAGAAAC TTCCAGCACA TTGGGGTGA GGGCCTGCCT | 1980 |
| CACTGGTCC CAGCTCCCG CTCCCTGTTAG CCCCCATGGGG CTGCCGGCT GGCGCCAGT | 2040 |
| TTCTGTTGCT GCCAAAGTAA TGTGGCTCTC TGCTGCCACC CTGCTGTGCT GAGGTGCGTA | 2100 |
| GCTGCACAGC TGGGGCTGG GGCCTCCCTC CCCTCTCTCA CCAGTCTCTA GGGCTGCCTG | 2160 |
| ACTGGAGGCC TTCCAAGGGG GTTTCAGTCT GGACTTATAC AGGGAGGCCA GAAGGGCTCC | 2220 |
| ATGCACTGGA ATGCGGGAC TCTGCAGGTG GATTACCCAG GCTCAGGGTT AACAGCTAGC | 2280 |
| CTCCTAGTT AGACACACCT AGAGAAGGGT TTTTGGAGC TGAATAAACT CAGTCACCTG | 2340 |
| TTTCTAGGAT GAAACACTCC TCCATGGGAT TTGAACATAT GACTTATTTG TAGGGGAAGA | 2400 |
| GTCTGAGGG GCAACACACA AGAACCAAGGT CCCCTCAGCC CACAGCACTG TCTTTTGCT | 2460 |
| | 2520 |

| | |
|---|------|
| GATCCACCCC CCTCTTACCT TTTATCAGGA TGTGGCCTGT TGTCCTTCT GTGCCATCA | 2580 |
| CAGAGACACA GGCATTTAAA TATTTAACCT ATTATTTAA CAAAGTAGAA GGGATCCAT | 2640 |
| TGCTAGCTT TCTGTGTTGG TGTCTAATAT TTGGGTAGGG TGGGGGATCC CCAACAATCA | 2700 |
| GGTCCCCCTGA GATAGCTGGT CATTGGGCTG ATCATTGCCA GAATCTTCTT CTCTGGGGT | 2760 |
| CTGGCCCCC AAAATGCCTA ACCCAGGACC TTGGAAATTCTACTCATCCC AAATGATAAT | 2820 |
| TCCAATGCT GTTACCCAAG GTTACGGGTG TGAGGAAGG TAGAGGGTGG GGCTTCAGGT | 2880 |
| CTCAACGGCT TCCCTAACCA CCCCTCTTCT CTTGGCCAG CCTGGTTCCC CCCACTTCCA | 2940 |
| CTCCCTCTA CTCTCTCTAG GACTGGGCTG ATGAAGGCAC TGCCAAAAT TTCCCTTAC | 3000 |
| CCCAACTTTC CCCTACCCCCC AACTTCCCCC ACCAGCTCCA CAACCCCTGTT TGGAGCTACT | 3060 |
| GCAGGACCAAG AAGCACAAAG TGCGGTTTCC CAAGCCTTGT TCCATCTCAG CCCCCAGAGT | 3120 |
| ATATCTGTG TGAGGAAATC TCACACAGAA ACTCAGGAGG ACCCCCTGCC TGAGCTAAGG | 3180 |
| GAGGTCTTAT CTCTCAGGGG GGGTTTAAGT GCCGTTGCA ATAATGTCGT CTTATTTATT | 3240 |
| TAGCGGGGTG AATATTTAT ACTGTAAGTG AGCAATCAGA GTATAATGTT TATGGTGACA | 3300 |
| AAATTAAAGG CTTCTTATA TGTTAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA | 3360 |
| AAAAAAAAAA AAAAAAAAAA AAAAAATAA AAAAAAAA | 3410 |

(2) INFORMATION FOR SEQ ID NO:111:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1289 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:111:

| | |
|--|------|
| AGCCAGGCCTT CCCTCTGCCT GCCCACTCAG TGGCAACACC CGGGAGCTGT TTTGTCTTT | 60 |
| GTGGAGCCTC AGCAGTCTCC TCTTCAGAA CTCACTGCCA AGAGCCCTGA ACAGGAGCCA | 120 |
| CCATCCAGTG CTTCAGCTTC ATTAAGACCA TGATGATCCT CTTCAATTG CTCATCTTC | 180 |
| TGTGTGGTGC AGCCCTGTG GCAGTGGCA TCTGGGTGC AATCGATGGG GCATCCCTTC | 240 |
| TGAAGATCTT CGGGCCACTG TCGTCCAGTG CCATGCAGT TGTCACAGTG GGCTACTTCC | 300 |
| TCATCGCAGC CGCGGTGTCG GTCTTGCTC TTGGTTCTT GGGCTGCTAT GGTGCTAAGA | 360 |
| CTGAGAGCAA GTGTGCCCTC GTGACGTTCT TCTTCATCCT CCTCCTCATC TTCATTGCTG | 420 |
| AGGTTGCAGC TGCTGTGGTC GCCTGGTGT ACACCACAAT GGCTGAGCAC TTCTGACGT | 480 |
| TGCTGGTAGT GCCTGCCATC AAGAAAGATT ATGGTTCCCA GGAAGACTTC ACTCAAGTGT | 540 |
| GGAACACCCAC CATGAAAGGG CTCAAGTGC GTGGCTTCAC CAACTATACG GATTTTGAGG | 600 |
| ACTCACCCCTA CTTCAAAGAG AACAGTGCCT TTCCCCCATT CTGGTGCATA GACAACGTCA | 660 |
| CCAACACAGC CAATGAAACC TGCACCAAGC AAAAGGCTCA CGACCAAAAAA GTAGAGGGTT | 720 |
| GCTTCAATCA GCTTTTGAT GACATCGGAA CTAATGCACT CACCGTGGGT GGTGTGGCAG | 780 |
| CTGGAATTGG GGGCCTCGAG CTGGCTGCCA TGATTGTGTC CATGTATCTG TACTGCAATC | 840 |
| TACAATAAGT CCACCTCTGC CTCTGCCACT ACTGCTGCCA CATGGGAACG GTGAAGAGGC | 900 |
| ACCCCTGGCAA GCAGCAGTGA TTGGGGGAGG GGACAGGATC TAACAATGTC ACTTGGGCCA | 960 |
| GAATGGACCT GCCCCTTCCTG CTCCAGACTT GGGGCTAGAT AGGGACCACT CCTTTAGCG | 1020 |
| ATGCCTGACT TTCCCTCCAT TGGTGGGTGG ATGGGTGGGG GGCATTCCAG AGCCTCTAAG | 1080 |
| GTAGCCAGTT CTGTTGCCCA TTCCCCCAGT CTATTAACCT CTTGATATGC CCCCTAGGCC | 1140 |
| TAGTGGTGAT CCCAGTGCTC TACTGGGGGA TGAGAGAAAG GCATTTATA GCCTGGGCAT | 1200 |
| AAGTGAAATC AGCAGAGCCT CTGGGTGGAT GTGTAGAAGG CACTTCAAAA TGCATAAAACC | 1260 |
| TGTTACAATG TTAAAAAAAAA AAAAAAAAAA | 1289 |

(2) INFORMATION FOR SEQ ID NO:112:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 315 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:112:

Met Val Phe Thr Val Arg Leu Leu His Ile Phe Thr Val Asn Lys Gln
1 5 10 15

Leu Gly Pro Lys Ile Val Ile Val Ser Lys Met Met Lys Asp Val Phe
20 25 30

Phe Phe Leu Phe Phe Leu Gly Val Trp Leu Val Ala Tyr Gly Val Ala
35 40 45

Thr Glu Gly Leu Leu Arg Pro Arg Asp Ser Asp Phe Pro Ser Ile Leu
50 55 60

Arg Arg Val Phe Tyr Arg Pro Tyr Leu Gln Ile Phe Gly Gln Ile Pro
65 70 75 80

Gln Glu Asp Met Asp Val Ala Leu Met Glu His Ser Asn Cys Ser Ser
85 90 95

Glu Pro Gly Phe Trp Ala His Pro Pro Gly Ala Gln Ala Gly Thr Cys
100 105 110

Val Ser Gln Tyr Ala Asn Trp Leu Val Val Leu Leu Val Ile Phe
115 120 125

Leu Leu Val Ala Asn Ile Leu Leu Val Asn Leu Leu Ile Ala Met Phe
130 135 140

Ser Tyr Thr Phe Gly Lys Val Gln Gly Asn Ser Asp Leu Tyr Trp Lys
145 150 155 160

Ala Gln Arg Tyr Arg Leu Ile Arg Glu Phe His Ser Arg Pro Ala Leu
165 170 175

Ala Pro Pro Phe Ile Val Ile Ser His Leu Arg Leu Leu Arg Gln
180 185 190

Leu Cys Arg Arg Pro Arg Ser Pro Gln Pro Ser Ser Pro Ala Leu Glu
195 200 205

His Phe Arg Val Tyr Leu Ser Lys Glu Ala Glu Arg Lys Leu Leu Thr
210 215 220

Trp Glu Ser Val His Lys Glu Asn Phe Leu Leu Ala Arg Ala Arg Asp
225 230 235 240

Lys Arg Glu Ser Asp Ser Glu Arg Leu Lys Arg Thr Ser Gln Lys Val
245 250 255

Asp Leu Ala Leu Lys Gln Leu Gly His Ile Arg Glu Tyr Glu Gln Arg
260 265 270

Leu Lys Val Leu Glu Arg Glu Val Gln Gln Cys Ser Arg Val Leu Gly
275 280 285

Trp Val Ala Glu Ala Leu Ser Arg Ser Ala Leu Leu Pro Pro Gly Gly
290 295 300

Pro Pro Pro Pro Asp Leu Pro Gly Ser Lys Asp
305 310 315

(2) INFORMATION FOR SEQ ID NO:113:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 553 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:113:

Met Val Gln Arg Leu Trp Val Ser Arg Leu Leu Arg His Arg Lys Ala
1 5 10 15

Gln Leu Leu Leu Val Asn Leu Leu Thr Phe Gly Leu Glu Val Cys Leu
20 25 30

Ala Ala Gly Ile Thr Tyr Val Pro Pro Leu Leu Leu Glu Val Gly Val
35 40 45

Glu Glu Lys Phe Met Thr Met Val Leu Gly Ile Gly Pro Val Leu Gly
50 55 60

Leu Val Cys Val Pro Leu Leu Gly Ser Ala Ser Asp His Trp Arg Gly
65 70 75 80

Arg Tyr Gly Arg Arg Pro Phe Ile Trp Ala Leu Ser Leu Gly Ile
85 90 95

Leu Leu Ser Leu Phe Leu Ile Pro Arg Ala Gly Trp Leu Ala Gly Leu
100 105 110

Leu Cys Pro Asp Pro Arg Pro Leu Glu Leu Ala Leu Ile Leu Gly
115 120 125

Val Gly Leu Leu Asp Phe Cys Gly Gln Val Cys Phe Thr Pro Leu Glu
130 135 140

Ala Leu Leu Ser Asp Leu Phe Arg Asp Pro Asp His Cys Arg Gln Ala
145 150 155 160

Tyr Ser Val Tyr Ala Phe Met Ile Ser Leu Gly Gly Cys Leu Gly Tyr
165 170 175

Leu Leu Pro Ala Ile Asp Trp Asp Thr Ser Ala Leu Ala Pro Tyr Leu
180 185 190

Gly Thr Gln Glu Glu Cys Leu Phe Gly Leu Leu Thr Leu Ile Phe Leu
195 200 205

Thr Cys Val Ala Ala Thr Leu Leu Val Ala Glu Glu Ala Ala Leu Gly
 210 215 220
 Pro Thr Glu Pro Ala Glu Gly Leu Ser Ala Pro Ser Leu Ser Pro His
 225 230 235 240
 Cys Cys Pro Cys Arg Ala Arg Leu Ala Phe Arg Asn Leu Gly Ala Leu
 245 250 255
 Leu Pro Arg Leu His Gln Leu Cys Cys Arg Met Pro Arg Thr Leu Arg
 260 265 270
 Arg Leu Phe Val Ala Glu Leu Cys Ser Trp Met Ala Leu Met Thr Phe
 275 280 285
 Thr Leu Phe Tyr Thr Asp Phe Val Gly Glu Gly Leu Tyr Gln Gly Val
 290 295 300
 Pro Arg Ala Glu Pro Gly Thr Glu Ala Arg Arg His Tyr Asp Glu Gly
 305 310 315 320
 Val Arg Met Gly Ser Leu Gly Leu Phe Leu Gln Cys Ala Ile Ser Leu
 325 330 335
 Val Phe Ser Leu Val Met Asp Arg Leu Val Gln Arg Phe Gly Thr Arg
 340 345 350
 Ala Val Tyr Leu Ala Ser Val Ala Ala Phe Pro Val Ala Ala Gly Ala
 355 360 365
 Thr Cys Leu Ser His Ser Val Ala Val Val Thr Ala Ser Ala Ala Leu
 370 375 380
 Thr Gly Phe Thr Phe Ser Ala Leu Gln Ile Leu Pro Tyr Thr Leu Ala
 385 390 395 400
 Ser Leu Tyr His Arg Glu Lys Gln Val Phe Leu Pro Lys Tyr Arg Gly
 405 410 415
 Asp Thr Gly Gly Ala Ser Ser Glu Asp Ser Leu Met Thr Ser Phe Leu
 420 425 430
 Pro Gly Pro Lys Pro Gly Ala Pro Phe Pro Asn Gly His Val Gly Ala
 435 440 445
 Gly Gly Ser Gly Leu Leu Pro Pro Pro Ala Leu Cys Gly Ala Ser
 450 455 460
 Ala Cys Asp Val Ser Val Arg Val Val Val Gly Glu Pro Thr Glu Ala
 465 470 475 480
 Arg Val Val Pro Gly Arg Gly Ile Cys Leu Asp Leu Ala Ile Leu Asp
 485 490 495
 Ser Ala Phe Leu Leu Ser Gln Val Ala Pro Ser Leu Phe Met Gly Ser
 500 505 510
 Ile Val Gln Leu Ser Gln Ser Val Thr Ala Tyr Met Val Ser Ala Ala
 515 520 525
 Gly Leu Gly Leu Val Ala Ile Tyr Phe Ala Thr Gln Val Val Phe Asp

| | | |
|-----|-----|-----|
| 530 | 535 | 540 |
|-----|-----|-----|

| |
|---|
| Lys Ser Asp Leu Ala Lys Tyr Ser Ala |
| 545 550 |

(2) INFORMATION FOR SEQ ID NO:114:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 241 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: protein

- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:114:

| | |
|---|-----|
| Met Gln Cys Phe Ser Phe Ile Lys Thr Met Met Ile Leu Phe Asn Leu | 15 |
| 1 5 10 | 15 |
| Leu Ile Phe Leu Cys Gly Ala Ala Leu Leu Ala Val Gly Ile Trp Val | 30 |
| 20 25 30 | 30 |
| Ser Ile Asp Gly Ala Ser Phe Leu Lys Ile Phe Gly Pro Leu Ser Ser | 45 |
| 35 40 45 | 45 |
| Ser Ala Met Gln Phe Val Asn Val Gly Tyr Phe Leu Ile Ala Ala Gly | 60 |
| 50 55 60 | 60 |
| Val Val Val Phe Ala Leu Gly Phe Leu Gly Cys Tyr Gly Ala Lys Thr | 80 |
| 65 70 75 80 | 80 |
| Glu Ser Lys Cys Ala Leu Val Thr Phe Phe Phe Ile Leu Leu Ile | 95 |
| 85 90 95 | 95 |
| Phe Ile Ala Glu Val Ala Ala Val Val Ala Leu Val Tyr Thr Thr | 110 |
| 100 105 110 | 110 |
| Met Ala Glu His Phe Leu Thr Leu Leu Val Val Pro Ala Ile Lys Lys | 125 |
| 115 120 125 | 125 |
| Asp Tyr Gly Ser Gln Glu Asp Phe Thr Gln Val Trp Asn Thr Thr Met | 140 |
| 130 135 140 | 140 |
| Lys Gly Leu Lys Cys Cys Gly Phe Thr Asn Tyr Thr Asp Phe Glu Asp | 160 |
| 145 150 155 160 | 160 |
| Ser Pro Tyr Phe Lys Glu Asn Ser Ala Phe Pro Pro Phe Cys Cys Asn | 175 |
| 165 170 175 | 175 |
| Asp Asn Val Thr Asn Thr Ala Asn Glu Thr Cys Thr Lys Gln Lys Ala | 190 |
| 180 185 190 | 190 |
| His Asp Gln Lys Val Glu Gly Cys Phe Asn Gln Leu Leu Tyr Asp Ile | 205 |
| 195 200 205 | 205 |
| Arg Thr Asn Ala Val Thr Val Gly Gly Val Ala Ala Gly Ile Gly Gly | 220 |
| 210 215 220 | 220 |

Leu Glu Leu Ala Ala Met Ile Val Ser Met Tyr Leu Tyr Cys Asn Leu
 225 230 235 240

Gln

(2) INFORMATION FOR SEQ ID NO:115:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 366 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:115:

| | | | |
|----------------------------------|--------------------|----------------------|-----|
| GCTCTTTCTC TCCCCTCCTC TGAATTTAAT | TCTTCAACT TGCAATTG | AAGGATTACA | 60 |
| CATTTCAGTG TGATGTATAT | TGTGTTGCAA | AAAAAAAAAA GTGCTTTGT | 120 |
| TTGGTTTGTG AATCCATCTT | GCTTTTCCC | CATTGGAAC | 180 |
| ACTGGTAGAA AAACATCTGA | AGAGCTAGTC | TATCAGCATC | 240 |
| TCTCAGAACC ATTTCACCCA | GACAGCCTGT | TGACAGGTGA | 300 |
| TCTCTACATG CATAACAAAC | CCTGCTCAA | ATTGGATGGT | 360 |
| TTAGTC | TCTGTACAT | AAAAGTCTGT | |
| | | GACTTGAAGT | 366 |

(2) INFORMATION FOR SEQ ID NO:116:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 282 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:116:

| | | |
|--|-----------------------|-----|
| ACAAAGATGA ACCATTCCT ATATTATAGC AAAATTTAAA | TCTACCGTA TTCTAATATT | 60 |
| GAGAAATGAG ATNAAACACA ATNTTATAAA | GTCTACTTAG AGAAGATCAA | 120 |
| AGACTTTACT ATTTTCATAT | GTGACCTCAA | 180 |
| ATACGTTAAA CAAAGGATAA | CTATTTAGT AACCTGGTTC | 240 |
| TCAATCTNGA ACTATCTANA | TTCTATTCC | 282 |

(2) INFORMATION FOR SEQ ID NO:117:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 305 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:117:

| | |
|---|-----|
| ACACATGTCG CTTCACTGCC TTCTTAGATG CTTCTGGTCA ACATANAGGA ACAGGGACCA | 60 |
| TATTTATCCT CCCTCTGAA ACAATTGCAA AATAANACAA AATATATGAA ACAATTGCAA | 120 |
| ATAAGGCAA AATATATGAA ACAACAGGT TCGAGATATT GGAAATCAGT CAATGAAGGA | 180 |
| TACTGATCCC TGATCACTGT CCTAATGCAG GATGTGGAA ACAGATGAGG TCACCTCTGT | 240 |
| GACTGCCCA GCTTACTGCC TGTAGAGAGT TTCTANGCTG CAGTCAGAC AGGGAGAAAT | 300 |
| TGGGT | 305 |

(2) INFORMATION FOR SEQ ID NO:118:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 71 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:118:

| | |
|---|----|
| ACCAAGGTGT NTGAATCTCT GACGTGGGA TCTCTGATTC CCCCACAAATC TGACTGGAAA | 60 |
| AANTCCTGGG T | 71 |

(2) INFORMATION FOR SEQ ID NO:119:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 212 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:119:

| | |
|--|-----|
| ACTCCGGTTG GTGTCAGCAG CACGTGGCAT TGAACATNGC AATGTGGAGC CAAACCACA | 60 |
| GAAATGGGG TGAAATTGGC CAACTTTCTA TNAACTTATG TTGGCAANTT TGCCACCAAC | 120 |
| AGTAAGCTGG CCCTTCTAAT AAAAGAAAAT TGAAAGGTTT CTCACTAAC GGAATTAANT | 180 |
| AATGGANTCA AGANACTCCC AGGCCTCAGC GT | 212 |

(2) INFORMATION FOR SEQ ID NO:120:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 90 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:120:

| | |
|---|----|
| ACTCGTTGCA NATCAGGGC CCCCCAGAGT CACCGTGCA, GGAGTCCTTC TGGTCTTGC | 60 |
| CTCCGCCGGC GCAGAACATG CTGGGGTGGT | 90 |

(2) INFORMATION FOR SEQ ID NO:121:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 218 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:121:

| | |
|--|-----|
| TGTANC GTGA ANACGACAGA NAGGGTTGTC AAAAATGGAG AANCCTTGAA GTCATTTGA | 60 |
| GAATAAGATT TGCTAAAAGA TTTGGGGCTA AAACATGGTT ATTGGGAGAC ATTTCTGAAG | 120 |
| ATATNCANGT AAATTANGGA ATGAATTCTAT GGTTCTTTG GGAATTCCCTT TACGATNGCC | 180 |
| AGCATANACT TCATGTGGGG ATANCAGCTA CCCTTGTA | 218 |

(2) INFORMATION FOR SEQ ID NO:122:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 171 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:122:

| | |
|---|-----|
| TAGGGGTGTA TGCAACTGTA AGGACAAAAA TTGAGACTCA ACTGGCTTAA CCAATAAAGG | 60 |
| CATTGTTAG CTCATGGAAC AGGAAGTCGG ATGGTGGGGC ATCTTCAGTG CTGCATGAGT | 120 |
| CACCAACCCG GCGGGGTGAT CTGTGCCACA GGTCCCTGTT GACAGTGCAG | 171 |

(2) INFORMATION FOR SEQ ID NO:123:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 76 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:123:

| | |
|---|----|
| TGTAGCGTGA AGACNACAGA ATGGTGTGTG CTGTGCTATC CAGGAACACA TTTATTATCA | 60 |
| TTATCAANTA TTGTGT | 76 |

(2) INFORMATION FOR SEQ ID NO:124:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 131 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

- (vi) ORIGINAL SOURCE:
- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:124:

| | |
|--|-----|
| ACCTTTCCCC AAGGCCAATG TCCTGTGTGC TAACTGGCCG GCTGCAGGAC AGCTGCAATT | 60 |
| CAATGTGCTG GGTCAATATGG AGGGGAGGAG ACTCTAAAAT AGCCAATTTT ATTCTCTTGG | 120 |
| TTAAGATTTG T | 131 |

(2) INFORMATION FOR SEQ ID NO:125:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 432 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

- (vi) ORIGINAL SOURCE:
- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:125:

| | |
|--|-----|
| ACTTTATCTA CTGGCTATGA AATAGATGGT GGAAAATTGC GTTACCAAAT ATACCACTGG | 60 |
| CTTGAAAAAG AGGTGATAGC TCTTCAGAGG ACTTGTAAGT TTTGCTCAGA TGCTGAAGAA | 120 |
| CTACAGTCTG CATTGGCAG AAATGAAGAT GAATTTGGAT TAAATGAGGA TGCTGAAGAT | 180 |
| TTGCCTCACCA AAACAAAAGT GAAACAACGT AGAGAAAATT TTCAGGAAAA AAGACAGTGG | 240 |
| CTCTTGAAGT ATCAGTCACT TTTGAGAATG TTTCTTAGTT ACTGCATACT TCATGGATCC | 300 |
| CATGGTGGGG GTCTTGCATC TGTAAGAATG GAATTGATTT TGCTTTGCA AGAATCTCAG | 360 |
| CAGGAAACAT CAGAACCACT ATTTCTAGC CCTCTGTCAG AGCAAACCTC AGTGCCTCTC | 420 |
| CTCTTGCTT GT | 432 |

(2) INFORMATION FOR SEQ ID NO:126:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 112 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

- (vi) ORIGINAL SOURCE:
- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:126:

| | |
|--|-----|
| ACACAACCTG AATAGTAAAA TAGAAACTGA GCTGAAATT CTAATTCACT TTCTAACCAT | 60 |
| AGTAAGAATG ATATTCccc CCAGGGATCA CCAAATATTG ATAAAAATTG GT | 112 |

(2) INFORMATION FOR SEQ ID NO:127:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 54 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:127:

| | |
|--|----|
| ACACGAAAC CACAAACAAG ATGGAAGCAT CAATCCACTT GCCAAGCACA GCAG | 54 |
|--|----|

(2) INFORMATION FOR SEQ ID NO:128:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 323 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:128:

| | |
|---|-----|
| ACCTCATTAG TAATTGTTTT GTTGTTCAT TTTTTCTAA TGCTCTCCCT CTACCAGCTC | 60 |
| ACCTGAGATA ACAGAATGAA AATGGAAGGA CAGCCAGATT TCTCCTTTGC TCTCTGCTCA | 120 |
| TTCTCTCTGA AGTCTAGGTT ACCCATTTCG GGGACCCATT ATAGGCAATA AACACAGTTC | 180 |
| CCAAAGCATT TGGACAGTTT CTTGTTGTGT TTTAGAATGG TTTCCCTTTT TCTTAGCCTT | 240 |
| TTCCTGCAAA AGGCTCACTC AGTCCCTTGC TTGCTCAGTG GACTGGGCTC CCCAGGGCCT | 300 |
| AGGCTGCCTT CTTTCCATG TCC | 323 |

(2) INFORMATION FOR SEQ ID NO:129:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 192 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:129:

| | |
|--|-----|
| ACATACATGT GTGTATATTT TTAAATATCA CTTTGTATC ACTCTGACTT TTTAGCATAC | 60 |
| TGAAAACACA CTAACATAAT TTNTGTGAAC CATGATCAGA TACAACCCAA ATCATTCA | 120 |

| | |
|--|------------|
| TAGCACATTC ATCTGTGATA NAAAGATAGG TGAGTTCAT TTCCCTTCACG TTGGCCAATG GATAAACAAA GT | 180 192 |
|--|------------|

(2) INFORMATION FOR SEQ ID NO:130:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 362 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

- (vi) ORIGINAL SOURCE:
- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:130:

| | |
|--|--|
| CCCTTTTTA TGGAATGAGT AGACTGTATG TTTGAANATT TANCCACAAC CTCTTGACA TATAATGACG CAACAAAAAG GTGCTGTTA GTCCTATGGT TCAGTTTATG CCCCTGACAA GTTTCCATTG TGGTTTGC CG ATCTTCTGGC TAATCGGGT ATCCTCCATG TTATTAGTAA TTCTGTATT CATTGGTTA ACGCCTGGT GATGTAACCT GCTANGAGGC TAACTTTATA CTTATTAAA AGCTCTTATT TTGTTGGTCA TAAAATGGCA ATTATGTGC AGCAGTTTATG TGCAGCGAGGA AGCACGTGTG GGTTGGTTGT AAAGCTCTTT GCTAATCTTA AAAAGTAATG GG | 60 120 180 240 300 360 362 |
|--|--|

(2) INFORMATION FOR SEQ ID NO:131:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 332 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

- (vi) ORIGINAL SOURCE:
- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:131:

| | |
|--|---------------------------------------|
| CTTTTGAAA GATCGTGTCC ACTCCTGTGG ACATCTGTT TTAATGGAGT TTCCCCATGCA GTANGACTGG TATGGTTGCA GCTGTCCAGA TAAAAACATT TGAAGAGCTC CAAAATGAGA GTTCTCCCAG GTTCCGCCCTG CTGCTCCAAG TCTCACCGAG AGCCTCTTT AGGAGGCATC TTCTGAACTA GATTAAGGCA GCTTGTAAAT CTGATGTGAT TTGGTTTATT ATCCAACCAA CTTCATCTG TTATCACTGG AGAAAGCCCA GACTCCCCAN GACNGTACG GATTGTGGC ATANAAGGAT TGGGTGAAGC TGGCGTTGTG GT | 60 120 180 240 300 332 |
|--|---------------------------------------|

(2) INFORMATION FOR SEQ ID NO:132:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 322 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

- (vi) ORIGINAL SOURCE:
- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:132:

| | |
|--|-----|
| ACTTTTGCCA TTTGTATAT ATAAACAATC TTGGGACATT CTCCTGAAAA CTAGGTGTCC | 60 |
| AGTGGCTAAG AGAACTCGAT TTCAAGCAAT TCTGAAAGGA AAACCAGCAT GACACAGAAAT | 120 |
| CTCAAATTCC CAAACAGGGG CTCTGTGGGA AAAATGAGGG AGGACCTTG TATCTCGGGT | 180 |
| TTTAGCAAGT TAAAATGAAN ATGACAGGAA AGGCTTATT ATCAACAAAG AGAAGAGTTG | 240 |
| GGATGCTTCT AAAAAAAACT TTGGTAGAGA AAATAGGAAT GCTNAATCCT AGGGAAGCCT | 300 |
| GTAACAACTC ACAATTGGTC CA | 322 |

(2) INFORMATION FOR SEQ ID NO:133:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 278 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:133:

| | |
|---|-----|
| ACAAGCCTTC ACAAGTTAA CTAAATTGGG ATTAATCTTT CTGTANTTAT CTGCATAATT | 60 |
| CTTGTTCCTTC TTTCATCTG GCTCCTGGGT TGACAATTTG TGGAAACAAC TCTATTGCTA | 120 |
| CTATTTAAA AAAATCACAA ATCTTCCCT TTAAGCTATG TTNAATTCAA ACTATTCTG | 180 |
| CTATTCCTGT TTGTCAAAG AAATTATATT TTCAAAAATA TGTNTATTTG TTGATGGGT | 240 |
| CCCACGAAAC ACTAATAAA ACCACAGAGA CCAGCCTG | 278 |

(2) INFORMATION FOR SEQ ID NO:134:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 121 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:134:

| | |
|---|-----|
| GT TTANAAAAA CTTGTTTAGC TCCATAGAGG AAAGAATGTT AAACTTTGTA TTTTAAAACA | 60 |
| TGATTCTCTG AGGTAAACT TGTTTCAA ATGTTATTT TACTTGTATT TTGCTTTGG | 120 |
| T | 121 |

(2) INFORMATION FOR SEQ ID NO:135:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 350 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:135:

| | |
|--|-----|
| ACTTANAACC ATGCCTAGCA CATCAGAAC CCTCAAAGAA CATCAGTATA ATCCCTATACC | 60 |
| ATANCAAGTG GTGACTGGTT AAGCGTGCAG CAAAGGTCACT CTGGCACATT ACTTGTTGTC | 120 |
| AAACTGATA CTTTTGTTCT AAGTAGGAAC TAGTATAACAG TNCCCTAGGAN TGTTACTCCA | 180 |
| GGGTGCCCCC CAACTCTGC AGCCGCTCCT CTGTGCCAGN CCCTGNAAGG AACTTTCGCT | 240 |
| CCACCTCAAT CAAGCCCTGG GCCATGCTAC CTGCAATTGG CTGAACAAAAC GTTTGCTGAG | 300 |
| TTCCCAAGGA TGCAAAAGCCT GGTGCTAAC TCCCTGGGGCG TCAACTCAGT | 350 |

(2) INFORMATION FOR SEQ ID NO:136:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 399 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:136:

| | |
|---|-----|
| TGTACCGTGA AGACGACAGA AGTTGCATGG CAGGGACAGG GCAGGGCCGA GCCCAGGGTT | 60 |
| GCTGTGATTG TATCCGAATA NTCTCGTGA GAAAAGATAA TGAGATGACG TGAGCAGCCT | 120 |
| GCAGACTTGT GCTCGCTTC AANAAGCCAG ACAGGAAGGC CCTGCCTGCC TTGGCTCTGA | 180 |
| CCTGGCGGCC AGCCAGGCCAG CCACAGGTGG CCTTCTTCCT TTTGTGGTGA CAACNCCAAG | 240 |
| AAAACTGCAG AGGCCCAAGGG TCAGGGTGTNA GTGGGTANGT GACCATAAAA CACCAGGTGC | 300 |
| TCCCAGGAAC CCGGGCAAAG GCCATCCCCA CCTACAGCCA GCATGCCAC TGGCGTGATG | 360 |
| GGTGCAGANG GATGAAGCAG CCAGNTGTTG TGCTGTGGT | 399 |

(2) INFORMATION FOR SEQ ID NO:137:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 165 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:137:

| | |
|--|-----|
| ACTGGTGTGG TNGGGGGTGA TGCTGGTGT ANAAGTTGAN GTGACTTCAN GATGGTGTGT | 60 |
| GGAGGAAGTG TGTGAACGTA GGGATGAGA NGTTTGGCC GTGCTAAATG AGCTTCGGGA | 120 |
| TTGGCTGGTC CCACTGGTGG TCACTGTCA TGGTGGGTT CCTGT | 165 |

(2) INFORMATION FOR SEQ ID NO:138:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 338 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:138:

| | |
|--|-----|
| ACTCACTGGA ATGCCACATT CACAACAGAA TCAGAGGTCT GTGAAAACAT TAATGGCTCC | 60 |
| TTAACCTCTC CAGTAAGAAC CAGGGACTTG AAATGGAAAC GTTAACAGCC ACATGCCAA | 120 |
| TGCTGGCAG TCTCCCAGT CTTCCACAGT GAAAGGGCTT GAGAAAAATC ACATCCAATG | 180 |
| TCATGTGTTT CCAGCCACAC CAAAAGGTGC TTGGGGTGGGA GGGCTGGGGG CATANANGGT | 240 |
| CANGCCTCAG GAAGCCTCAA GTTCATTCA GCTTGCCAC TGTACATTCC CCATNTTTAA | 300 |
| AAAAGCTGAT GCCTTTTTT TTTTTTTTG TAAAATTTC | 338 |

(2) INFORMATION FOR SEQ ID NO:139:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 382 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:139:

| | |
|--|-----|
| GGGAATCTTG GTTTTGGCA TCTGGTTGC CTATAGCCGA GGCCACTTTG ACAGAACAAA | 60 |
| GAAAGGGACT TCGAGTAAGA AGGTGATTAA CAGCCAGCCT AGTGCCCGAA GTGAAGGAGA | 120 |
| ATTCAAACAG ACCTCGTCAT TCCTGGTGT AGCCTGGTCG GCTCACCGCC TATCATCTGC | 180 |
| ATTTCCTTA CTCAGGTGCT ACCGGACTCT GGCCCCGTAT GTCTGTAGTT TCACAGGATG | 240 |
| CCTTATTGTG CCTCTACACC CCACAGGGCC CCCTACTCTC TCGGATGTGT TTTTAATAAT | 300 |
| GTCAAGCTATG TGCCCCATCC TCCTTCATGC CCTCCCTCCC TTTCCTACCA CTGCTGAGTG | 360 |
| GGCTGGAAC TGTAAAGT GT | 382 |

(2) INFORMATION FOR SEQ ID NO:140:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 200 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:140:

| | |
|---|-----|
| ACCAAANCTT CTTTCTGTTG TGTTNGATTT TACTATAGGG GTTNGCTTN TTCTAAANAT | 60 |
| ACTTTTCATT TAACANCTTT TGTTAAGTGT CAGGCTGCAC TTTGCTCCAT ANAATTATTG | 120 |
| TTTCACATT TCAACTTGTA TGTGTTGTC TCTTANAGCA TTGGTGAAT CACATATTTC | 180 |
| ATATTCAAGCA TAAAGGAGAA | 200 |

(2) INFORMATION FOR SEQ ID NO:141:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 335 base pairs
 (B) TYPE: nucleic acid

(C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:141:

| | |
|--|-----|
| ACTTATTTT CAAAACACTC ATATGTCGA AAAAACACAT AGAAAAATAA AGTTTGGTGG | 60 |
| GGGTGCTGAC TAAACCTCAA GTCACAGACT TTTATGTGAC AGATTGGAGC AGGGTTTGT | 120 |
| ATGCATGTAG AGAACCCAAA CTAATTATT AAACAGGATA GAAACAGGCT GTCTGGGTGA | 180 |
| AATGGTTCTG AGAACCATCC AATTCACTG TCAGATGCTG ATANACTAGC TCTTCAGATG | 240 |
| TTTTCTTAC AGTTCAGAGA TNGGTTAATG ACTANTCCA ATGGGGAAAA AGCAAGATGG | 300 |
| ATTACACAAAC CAAGTAATT TAAACAAAGA CACTT | 335 |

(2) INFORMATION FOR SEQ ID NO:142:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 459 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:142:

| | |
|--|-----|
| ACCAGGTTAA TATTGCCACA TATATCCTT CCAATTGCGG GCTAAACAGA CGTGTATTTA | 60 |
| GGGTGTTTA AAGACAACCC AGCTTAATAT CAAGAGAAAT TGTGACCTTT CATGGAGTAT | 120 |
| CTGATGGAGA AACAACTGAG TTTTGACAAA TCTTATTTTA TTCAGATAGC AGTCTGATCA | 180 |
| CACATGGTCC ACAACACACTC AAATAATAAA TCAAATATNA TCAGATGTTA AAGATTGGTC | 240 |
| TTCAAACATC ATAGCCAATG ATGCCCCGCT TGCCCTATAAT CTCTCCGACA TAAAACCACA | 300 |
| TCAACACCTC AGTGGCCACC AAACCATTC GCACAGCTTC CTTAACTGTG AGCTGTTTGA | 360 |
| AGCTACCAAGT CTGAGCACTA TTGACTATNT TTTTCANGCT CTGAATAGCT CTAGGGATCT | 420 |
| CAGCANGGTT GGGAGGAACC AGCTCAACCT TGGCGTANT | 459 |

(2) INFORMATION FOR SEQ ID NO:143:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 140 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:143:

| | |
|--|-----|
| ACATTTCCCTT CCACCAAGTC AGGACTCCTG GCTTCTGTGG GAGTTCTTAT CACCTGAGGG | 60 |
| AAATCCAAAC AGTCTCTCCT AGAAAGGAAT AGTGTACCA ACCCCACCCA TCTCCCTGAG | 120 |
| ACCATCCGAC TTCCCTGTGT | 140 |

(2) INFORMATION FOR SEQ ID NO:144:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 164 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:144:

| | |
|--|-----|
| ACTTCAGTAA CAACATACAA TAACAACATT AAGTGATAT TGCCATCTT GTCATTTCT | 60 |
| ATCTATACCA CTCTCCCTTC TGAAAACAAN AATCACTANC CAATCACTTA TACAAATTG | 120 |
| AGGCAATTAA TCCATATTTG TTTCAATAA GGAAAAAAAG ATGT | 164 |

(2) INFORMATION FOR SEQ ID NO:145:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 303 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:145:

| | |
|--|-----|
| ACGTAGACCA TCCAACATTG TATTTGTAAT GGCAAACATC CAGNAGCAAT TCCTAACAA | 60 |
| ACTGGGGGT ATTATACCC AATTATCCA TTCATTAACA TGCCCTCTC CTCAGGCTAT | 120 |
| GCAGGACAGC TATCATAAGT CGGCCAGGC ATCCAGATAC TACCATTTGT ATAAACTTCA | 180 |
| GTAGGGAGT CCATCCAAGT GACAGGTCTA ATCAAAGGAG GAAATGGAAC ATAAGCCAG | 240 |
| TAGTAAATN TTGCTTAGCT GAAACAGCCA CAAAAGACTT ACCGCCGTGG TGATTACCAT | 300 |
| CAA | 303 |

(2) INFORMATION FOR SEQ ID NO:146:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 327 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:146:

| | |
|--|-----|
| ACTGCAGCTC AATTAGAAGT GGTCTCTGAC TTTCATCANC TTCTCCCTGG GCTCCATGAC | 60 |
| ACTGGCCTGG AGTGACTCAT TGCTCTGTT GGTTGAGAGA GCTCCTTTGC CAACAGGCCT | 120 |
| CCAAGTCAGG GCTGGGATTG GTTTCCTTTC CACATCTAG CAACAATATG CTGGCCACTT | 180 |
| CCTGAACAGG GAGGGTGGGA GGAGCCAGCA TGGAAACAAGC TGCCACTTTC TAAAGTAGCC | 240 |
| AGACTTGCCC CTGGGCTGTG CACACCTACT GATGACCTTC TGTGCCTGCA GGATGGAATG | 300 |
| TAGGGGTGAG CTGTGTGACT CTATGGT | 327 |

(2) INFORMATION FOR SEQ ID NO:147:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 173 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:147:

| | |
|---|-----|
| ACATTTGTTT TTTGAGATAA AGCATTGANA GAGCTCTCCT TAACGTGACA CAATGGAAGG | 60 |
| ACTGGAACAC ATACCCACAT CTTTGTCTG AGGGATAATT TTCTGATAAA GTCTTGCTGT | 120 |
| ATATTCAAGC ACATATGTTA TATATTATTC AGTTCCATGT TTATAGCCTA GTT | 173 |

(2) INFORMATION FOR SEQ ID NO:148:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 477 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:148:

| | |
|--|-----|
| ACAACCAACT TATCTCATCG AATTTTAAC CCAAACTCAC TCACTGTGCC TTTCTATCCT | 60 |
| ATGGGATATA TTATTTGATG CTCCATTCTA TCACACATAT ATGAATAATA CACTCATACT | 120 |
| GCCCTACTAC CTGCTGCAAT AACACATTC CCTTCTGTGTC CTGACCCCTGA AGCCATTGGG | 180 |
| GTGGTCCTAG TGGCCATCA TCCANGCTG CACCTTGAGC CCTTGAGCTC CATTGCTCAC | 240 |
| NCCANCCAC CTCACCGACC CCATCCTCTT ACACAGCTAC CTCCCTGCTC TCTAACCCCA | 300 |
| TAGATTATNT CCAAATTCAAG TCAATTAAGT TACTATTAAC ACTCTACCCG ACATGTCCAG | 360 |
| CACCACTGGT AAGCCTCTC CAGCCAACAC ACACACACAC ACACNCACAC ACACACATAT | 420 |
| CCAGGCACAG GCTACCTCAT CTTCACAATC ACCCCTTAA TTACCATGCT ATGGTGG | 477 |

(2) INFORMATION FOR SEQ ID NO:149:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 207 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:149:

| | |
|---|-----|
| ACAGTTGTAT TATAATATCA AGAAATAAAC TTGCAATGAG AGCATTAAAG AGGGAAGAAC | 60 |
| TAACGTATTT TAGAGAGCCA AGGAAGGTTT CTGTGGGGAG TGGGATGTAA GGTGGGGCT | 120 |

GATGATAAAAT AAGAGTCAGC CAGGTAAGTG GGTGGTGTGG TATGGGCACA GTGAAGAAC 180
 TTTCAGGCAG AGGGAACAGC AGTGAAA 207

(2) INFORMATION FOR SEQ ID NO:150:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 111 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:150:

ACTTGATT T CATTGCTGCT CTGATGGAAA CCCAACTATC TAATTTAGCT AAAACATGGG 60
 CACTAAATG TGGTCAGTGT TTGGACTTGT TAACTANTGG CATCTTGAG T 111

(2) INFORMATION FOR SEQ ID NO:151:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 196 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:151:

AGCCGGCAG GTCATATTGA ACATTCCAGA TACCTATCAT TACTCGATGC TGTTGATAAC 60
 AGCAAGATGG CTTTGAACTC AGGGTCACCA CCAGCTATTG GACCTTACTA TGAAAACCAT 120
 GGATACCAAC CGGAAAACCC CTATCCCGCA CAGCCCCTG TGGTCCCCAC TGTCTACGAG 180
 GTGCATCCGG CTCAGT 196

(2) INFORMATION FOR SEQ ID NO:152:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 132 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:152:

ACAGCACTTT CACATGTAAG AAGGGAGAAA TTCCTAAATG TAGGAGAAAG ATAACAGAAC 60
 CTTCCCCCTTT TCATCTAGTG GTGGAAACCT GATGCTTTAT GTTGACAGGA ATAGAACAG 120
 GAGGGAGTTT GT 132

(2) INFORMATION FOR SEQ ID NO:153:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 285 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:153:

| | |
|---|-----|
| ACAAANACCCA NGANAGGCCA CTGGCCGTGG TGTCAATGGCC TCCAAACATG AAAGTGTCA | 60 |
| CTTCCTGCTCT TATGTCCCTCA TCTGACAAC TCTTACCAATT TTTATCCTCG CTCAGCAGGA | 120 |
| GCACATCAAT AAAGTCCAAA GTCTTGGACT TGGCCTTGGC TTGGAGGAAG TCATCAACAC | 180 |
| CCTGGCTAGT GAGGGTGCAG CGCCGCTCT GGATGACGGC ATCTGTGAAG TCGTGCACCA | 240 |
| GTCTGCAGGC CCTGTGGAAG CGCCGTCCAC ACGGAGTNAG GAATT | 285 |

(2) INFORMATION FOR SEQ ID NO:154:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 333 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:154:

| | |
|--|-----|
| ACCACAGTCC TGTGGGCCA GGGCTTCATG ACCCTTTCTG TGAAAAGCCA TATTATCACC | 60 |
| ACCCCAAATT TTTCCTTAAA TATCTTTAAC TGAAGGGTC AGCCTTGA CTGCAAAGAC | 120 |
| CCTAACCGGG TTACACAGCT AACTCCCCTGATT TGTAATTG CTGCTGCCTG | 180 |
| ATTGGCACAG GAGTCGAAGG TGTTCAGCTC CCCTCTCCG TGGAACGAGA CTCTGATTG | 240 |
| AGTTTCACAA ATTCTCGGGC CACCTCGTCA TTGCTCTCT GAAATAAAAT CCGGAGAATG | 300 |
| GTCAGGCCCTG TCTCATCCAT ATGGATCTTC CGG | 333 |

(2) INFORMATION FOR SEQ ID NO:155:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 308 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:155:

| | |
|---|-----|
| ACTGGAAATA ATAAAACCCA CATCACAGTG TTGTGTCAAA GATCATCAGG GCATGGATGG | 60 |
| GAAAGTGCTT TGGGAACGTG AAGTGCCTA ACACATGATC GATGATTTT GTTATAATAT | 120 |
| TTGAATCACG GTGCATACAA ACTCTCTGC CTGCTCTCC TGGCCCCAG CCCCAGCCC | 180 |
| ATCACAGCTC ACTGCTCTGT TCATCCAGGC CCAGCATGTA GTGGCTGATT CTTCTGGCT | 240 |

| | |
|--|-----|
| GCTTTAGCC TCCANAAGTT TCTCTGAAGC CAACCAAACC TCTANGTGTA AGGCATGCTG | 300 |
| GCCCTGGT | 308 |

(2) INFORMATION FOR SEQ ID NO:156:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 295 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:156:

| | |
|---|-----|
| ACCTTGCTCG GTGCTTGGAA CATATTAGGA ACTCAAAATA TGAGATGATA ACAGTGCCTA | 60 |
| TTATTGATTA CTGAGAGAAC TGTTAGACAT TTAGTTGAAG ATTTCTACA CAGGAACGTGA | 120 |
| GAATAGGAGA TTATGTTGG CCCTCATATT CTCTCTTATC CTCCCTGCCT CATTCTATGT | 180 |
| CTAATATATT CTCATCAAA TAAGGTTAGC ATAATCAGGA AATCGACCAA ATACCAATAT | 240 |
| AAAACCAGAT GTCTATCCTT AAGATTTCA AATAGAAAAC AAATTAACAG ACTAT | 295 |

(2) INFORMATION FOR SEQ ID NO:157:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 126 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:157:

| | |
|--|-----|
| ACAAGTTAA ATAGTGTGT CACTGTGCAT GTGCTGAAAT GTGAAATCCA CCACATTCT | 60 |
| GAAGAGCAAA ACAAAATTCTG TCATGTAATC TCTATCTTGG GTCGTGGGTA TATCTGTCCC | 120 |
| CTTAGT | 126 |

(2) INFORMATION FOR SEQ ID NO:158:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 442 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:158:

| | |
|---|-----|
| ACCCACTGGT CTTGGAAACA CCCATCCTTA ATACGATGAT TTTCTGTGCG TGTGAAAATG | 60 |
| AANCCAGCAG GCTGCCCTA GTCAGTCCTT CCTTCCAGAG AAAAAGAGAT TTGAGAAAGT | 120 |
| GCCTGGGTAA TTCACCATTAA ATTTCTCCC CCAAACCTCTC TGAGTCTTCC CTTAATATT | 180 |

100

| | |
|--|-----|
| CTGGTGGTTC TGACCAAAGC AGGTCAATGGT TTGTTGAGCA TTTGGGATCC CAGTGAAGTA | 240 |
| NATGTTGTA GCCTTGATA CTTAGGCCCTT CCCACGCACA AACGGAGTGG CAGAGTGGTC | 300 |
| CCAACCTGT TTTCAGTC CACGTAGACA GATTACAGT GCGGAATTCT GGAAGCTGGA | 360 |
| NACAGACGGG CTCTTGAG AGCCGGGACT CTGAGANGGA CATGAGGGCC TCTGCCCTCG | 420 |
| TGTTCAATTCT CTGATGTCCT GT | 442 |

(2) INFORMATION FOR SEQ ID NO:159:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 498 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: cDNA

- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:159:

| | |
|--|-----|
| ACTTCCAGGT AACGTTGTTG TTTCCGTGAA GCCTGAAC TG ATGGGTGACG TTGTAGGTTC | 60 |
| TCCAACAAGA ACTGAGGTTG CAGAGCGGGT AGGGAAAGGT GCTGTTCCAG TTGCACCTGG | 120 |
| GCTGCTGTGG ACTGTGTTG ATTCCCTACT ACAGGCCAAG GTTGTGGAAC TGGCANAAAG | 180 |
| GTGTTGTTGTT GGANTTGAGC TCAGGGCGCT GTGGTAGGTT GTGGGCTCTT CAACAGGGGC | 240 |
| TGCTGTGGTGC CGGGGANGTG AANGTGTGTT GTCACTTGAG CTTGGCCAGC TCTGGAAAGT | 300 |
| ANTANATTCT TCCGTGAGGC CAGCGCTTG TGAGCTGGCA NGGGTCANTG TTGTGTGTA | 360 |
| CGAACAGGTG CTGCTGTGGG TGGGTGTANA TCCTCCACAA AGCTGAAGT TATGGTGTCTN | 420 |
| TCAGGTAANA ATGTGGTTTC AGTGTCCCTG GGCNGCTGTG GAAGGTTGTA NATTGTCA | 480 |
| AAGGGATAAA GCTGTGGT | 498 |

(2) INFORMATION FOR SEQ ID NO:160:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 380 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: cDNA

- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:160:

| | |
|---|-----|
| ACCTGCATCC AGCTTCCCTG CCAAACCTCAC AAGGAGACAT CAAACCTCTAG ACAGGGAAAC | 60 |
| AGCTTCAGGA TACTTCCAGG AGACAGAGCC ACCAGCAGCA AAACAAATAT TCCCATGCCT | 120 |
| GGAGCATGGC ATAGAGGAAG CTGANAAATG TGGGGTCTGA GGAAGCCATT TGAGTCTGGC | 180 |
| CACTAGACAT CTCATCAGCC ACTTGTGTGA AGAGATGCC CATGACCCCCA GATGCCTCTC | 240 |
| CCACCCCTAC CTCCATCTCA CACACTTGAG CTITCCACTC TGATATAATTG TAACATCCTG | 300 |
| GAGAAAAATG GCAGTTTGAC CGAACCTGTT CACAACGGTA GAGGCTGATT TCTAACGAAA | 360 |
| CTTGTAGAAT GAAGCCTGGA | 380 |

(2) INFORMATION FOR SEQ ID NO:161:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 114 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:161:

| | |
|--|-----|
| ACTCCACATC CCCTCTGAGC AGGC GGTTGT CGTTCAAGGT GTATTTGGCC TTGCCTGTCA | 60 |
| CACTGTCCAC TGCCCCCTTA TCCACTTGTT GCTTAATCCC TCGAAAGAGC ATGT | 114 |

(2) INFORMATION FOR SEQ ID NO:162:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 177 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:162:

| | |
|---|-----|
| ACTTTCTGAA TCGAATCAAA TGATACTTAG TGTAGTTTA ATATCCTCAT ATATATCAAA | 60 |
| GTTTACTAC TCTGATAATT TTGTAAACCA GGTAACCGAGA ACATCCAGTC ATACAGCTTT | 120 |
| TGGTGATATA TAACTGGCA ATAACCCAGT CTGGTGATAC ATAAAACATAC TCACTGT | 177 |

(2) INFORMATION FOR SEQ ID NO:163:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 137 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:163:

| | |
|---|-----|
| CATTATACA GACAGGCCGTG AAGACATTCA CGACAAAAAC GCGAAATTCT ATCCCGTGAC | 60 |
| CANAGAAGGC AGCTACGGCT ACTCCTACAT CCTGGCGTGG GTGGCCTTCG CCTGCACCTT | 120 |
| CATCAGCGGC ATGATGT | 137 |

(2) INFORMATION FOR SEQ ID NO:164:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 469 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:164:

| | |
|--|-----|
| CTTATCACAA TGAATGTTCT CCTGGGCAGC GTTGTGATCT TTGCCACCTT CGTGACTTTA | 60 |
| TGCAATGCAT CATGCTATT CATACTTAAT GAGGGAGGTC CAGGAGATT ACCAGGAAA | 120 |
| TGCATGGATC TCAAAGGAAA CAAACACCCA ATAAACTCGG AGTGGCAGAC TGACAACTGT | 180 |
| GAGACATGCA CTTGCTACGA AACAGAAATT TCATGTTGCA CCCTTGTTC TACACCTGTG | 240 |
| GGTTATGACA AAGACAACGT CCAAAGAACCC TTCAAGAAGG AGGACTGCAA GTATATCGTG | 300 |
| GTGGAGAAGA AGGACCCAAA AAAAGACCTGT TCTGTCAGTG AATGGATAAT CTAATGTGCT | 360 |
| TCTAGTAGGC ACAGGGCTCC CAGGCCAGGC CTCATTCTCC TCTGGCCTCT AATAGTCAAT | 420 |
| GATTGTGTAG CCATGCCTAT CAGTAAAAAG ATNTTGAGC AAACACTTT | 469 |

(2) INFORMATION FOR SEQ ID NO:165:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 195 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:165:

| | |
|---|-----|
| ACAGTTTTTT ATANATATCG ACATTGCCGG CACTTGTGTT CAGTTTCATA AAGCTGGTGG | 60 |
| ATCCGCTGTC ATCCACTATT CCTTGGCTAG AGTAAAATT ATTCTTATAG CCCATGTCCC | 120 |
| TGCAGGCCGC CCGCCCGTAG TTCTCGTTCC AGTCGTCTTG GCACACAGGG TGCCAGGACT | 180 |
| TCCTCTGAGA TGAGT | 195 |

(2) INFORMATION FOR SEQ ID NO:166:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 383 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:166:

| | |
|--|-----|
| ACATCTTAGT AGTGTGGCAC ATCAGGGGGC CATCAGGGTC ACAGTCACTC ATAGCCTCGC | 60 |
| CGAGGTCGGA GTCCACACCA CCGGTGTAAG TGTCCTCAAT CCTGGGCTTG GCGCCACCT | 120 |
| TTGGAGAAGG CATATGCTGC ACACACATGT CCACAAAGCC TGTAACCTCG CCAAAGAATT | 180 |
| TTTGCAGACC AGCCTGAGCA AGGGCGGAT GTTCAGCTTC AGCTCCTCCT TCGTCAGGTG | 240 |
| GATGCCAACC TCGTCTANGG TCCGTGGGAA GCTGGTGTCC ACNTCACCTA CAACCTGGGC | 300 |
| GANGATCTTA TAAAGAGGGCT CCNAGATAAA CTCCACGAAA CTTCTCTGGG AGCTGCTAGT | 360 |
| NGGGCCTTT TTGGTGAACT TTC | 383 |

(2) INFORMATION FOR SEQ ID NO:167:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 247 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:167:

| | |
|---|-----|
| ACAGAGCCAG ACCTTGGCCA TAAATGAANC AGAGATTAAG ACTAAACCCC AAGTCGANAT | 60 |
| TGGAGCAGAA ACTGGAGCAA GAAGTGGGCC TGGGGCTGAA GTAGAGACCA AGGCCACTGC | 120 |
| TATANCCATA CACAGAGCCA ACTCTCAGGC CAAGGCNATG GTTGGGGCAG ANCCAGAGAC | 180 |
| TCAATCTGAN TCCAAAGTGG TGGCTGGAAC ACTGGTCATG ACANAGGCAG TGACTCTGAC | 240 |
| TGANGTC | 247 |

(2) INFORMATION FOR SEQ ID NO:168:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 273 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:168:

| | |
|---|-----|
| ACTTCTAACT TTTCTAGAAG TGGAAGGATT GTANTCATCC TGAAAATGGG TTTACTTCAA | 60 |
| AATCCCTCAN CCTTGTCTT CACNACTGTC TATACTGANA GTGTCTGTT TCCACAAAGG | 120 |
| GCTGACACCT GAGCCTGNAT TTTCACTCAT CCCTGAGAAG CCCTTCCAG TAGGGTGGGC | 180 |
| AATTCCCAAC TTCTTGCCA CAAGCTTCCC AGGTTTCTC CCCTGGAAAA CTCCAGCTTG | 240 |
| AGTCCCAGAT ACACCATGG GCTGCCCTGG GCA | 273 |

(2) INFORMATION FOR SEQ ID NO:169:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 431 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:169:

| | |
|--|-----|
| ACAGCCTTGG CTTCCCCAAA CTCCACAGTC TCAGTGCAGA AAGATCATCT TCCAGCAGTC | 60 |
| AGCTCAGACC AGGGTCAAAG GATGTGACAT CAACAGTTTC TGGTTTCAGA ACAGGTTCTA | 120 |
| CTACTGTCAA ATGACCCCCC ATACTTCCTC AAAGGCTGTG GTAAGTTTG CACAGGTGAG | 180 |
| GGCAGCAGAA AGGGGGTANT TACTGATGGA CACCACCTTC TCTGTATACT CCACACTGAC | 240 |
| CTTGCCATGG GCAAAGGCC CTACCACAAA AACAAATAGGA TCACTGCTGG GCACCCAGCTC | 300 |
| ACGCACATCA CTGACAACCG GGATGGAAAA AGAANTGCCA ACTTTCATAC ATCCAACCTGG | 360 |
| AAAGTGATCT GATACTGGAT TCTTAATTAC CTTCAAAAGC TTCTGGGGC CATCAGCTGC | 420 |
| TCGAACACTG A | 431 |

(2) INFORMATION FOR SEQ ID NO:170:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 266 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:170:

| | |
|--|-----|
| ACCTGTGGGC TGGGCTGTTA TGCCCTGTGCC GGCTGCTGAA AGGGAGTTCA GAGGTGGAGC | 60 |
| TCAAGGGACT CTGCAGGAT TTTGCCAANC CTCTCCANAG CANAGGGAGC AACCTACACT | 120 |
| CCCCCGCTAGA AAGACACCAAG ATTGGAGTCC TGGGAGGGGG AGTTGGGTG GGCATTTGAT | 180 |
| GTATACTTGT CACCTGAATG AANGAGCCAG AGAGGAANGA GACGAANATG ANATTGGCCT | 240 |
| TCAAAGCTAG GGGTCTGGCA GGTGGA | 266 |

(2) INFORMATION FOR SEQ ID NO:171:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1248 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:171:

| | |
|---|------|
| GGCAGCCAAA TCATAAACGG CGAGGACTGTC AGCCCGCACT CGCAGCCCTG GCAGGGGGCA | 60 |
| CTGGTCATGG AAAACGAATT GTTCTGCTCG GGCCTCCTGG TGCATCCGCA GTGGGTGCTG | 120 |
| TCAGCCGCAC ACTGTTTCCA GAAGTGAGTG CAGAGCTCCT ACACCACATCGG GCTGGGCCTG | 180 |
| CACAGTCTTG AGGCCGACCA AGAGCCAGGG AGCCAGATGG TGGGAGGCCAG CCTCTCCGTA | 240 |
| CGGCACCCAG AGTACAACAG ACCCTTGCTC GCTAACGACC TCATGCTCAT CAAGTTGGAC | 300 |
| GAATCCGTGT CCGAGTCTGA CACCATCCGG AGCATCAGCA TTGCTTCGCA GTGCCCTTAC | 360 |
| CGGGGAACT CTTCGCTCGT TTCTGGCTGG GGTCCTGCTGG CGAACGGCAG ATGCTTAC | 420 |
| GTGCTGCAGT CGGTGAACGT GTCCGGTGGT TCTGAGGGAGG TCTGAGTAA GCTCTATGAC | 480 |
| CCGCTGTACCC ACCCCAGCAT GTTCTGCGCC GGCAGGGGC AAGAGCAGAA GGACTCCTGC | 540 |
| AACGGTGAAT CTGGGGGGCC CTCGATCTGC AACGGTACT TGCAAGGCCT TGTGTCTTC | 600 |
| GGAAAAGCCC CGTGTGGCCA AGTTGGCTG CCAGGTGCT ACACAAACCT CTGCAAATT | 660 |
| ACTGAGTGGAA TAGAGAAAAC CGTCAGGCC AGTTAACTCT GGGGACTGGG AACCCATGAA | 720 |
| ATTGACCCCCC AAATAACATCC TGCGGAAGGA ATTCAAGGAAT ATCTGTTCCC AGCCCTCCT | 780 |
| CCCTCAGGCC CAGGAGTCCA GGCCCCCAGC CCCTCCCTCC TCAAACCAAG GGTACAGATC | 840 |
| CCCAGCCCCCT CCTCCCTCAG ACCCAGGAGT CCAGACCCCC CAGCCCCCTCC TCCCTCAGAC | 900 |
| CCAGGAGTCC AGCCCCCTCCT CCCTCAGACC CAGGAGTCCA GACCCCCCAG CCCCTCCCTCC | 960 |
| CTCAGACCCA GGGGTCAGG CCCCCAACCC CTCCTCCCTC AGACTCAGAG GTCCAAGCCC | 1020 |
| CCAACCCNTC ATTCCCCAGA CCCAGAGGTC CAGGTCCAG CCCCTCCTCC CTCAGACCCA | 1080 |
| GCGGTCCAAT GCCACCTAGA CTNTCCCTGT ACACAGTGCC CCCTTGCCG ACGTTGACCC | 1140 |
| AACCTTACCA GTTGGTTTTT CATTGTTNGT CCCTTCCCC TAGATCCAGA AATAAAGTTT | 1200 |
| AAGAGAAGNG CAAAAAAA AAAAAAAA AAAAAAAA AAAAAAAA AAAAAAAA | 1248 |

(2) INFORMATION FOR SEQ ID NO:172:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 159 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:172:

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Val | Glu | Ala | Ser | Leu | Ser | Val | Arg | His | Pro | Glu | Tyr | Asn | Arg | Pro |
| 1 | | | | | 5 | | | 10 | | | | | | 15 | |
| ? | | | | | | | | | | | | | | | |
| Leu | Leu | Ala | Asn | Asp | Leu | Met | Leu | Ile | Lys | Leu | Asp | Glu | Ser | Val | Ser |
| | | | | | 20 | | | 25 | | | | | | 30 | |
| ? | | | | | | | | | | | | | | | |
| Glu | Ser | Asp | Thr | Ile | Arg | Ser | Ile | Ser | Ile | Ala | Ser | Gln | Cys | Pro | Thr |
| | | | | | 35 | | | 40 | | | | | | 45 | |
| Ala | Gly | Asn | Ser | Cys | Leu | Val | Ser | Gly | Trp | Gly | Leu | Leu | Ala | Asn | Gly |
| | | | | | 50 | | 55 | | | | | | | 60 | |
| Arg | Met | Pro | Thr | Val | Leu | Gln | Cys | Val | Asn | Val | Ser | Val | Val | Ser | Glu |
| | | | | | 65 | | 70 | | 75 | | | | | 80 | |
| Glu | Val | Cys | Ser | Lys | Leu | Tyr | Asp | Pro | Leu | Tyr | His | Pro | Ser | Met | Phe |
| | | | | | 85 | | | 90 | | | | | | 95 | |
| Cys | Ala | Gly | Gly | Gly | Gln | Xaa | Gln | Xaa | Asp | Ser | Cys | Asn | Gly | Asp | Ser |
| | | | | | 100 | | | 105 | | | | | | 110 | |
| Gly | Gly | Pro | Leu | Ile | Cys | Asn | Gly | Tyr | Leu | Gln | Gly | Leu | Val | Ser | Phe |
| | | | | | 115 | | | 120 | | | | | | 125 | |
| Gly | Lys | Ala | Pro | Cys | Gly | Gln | Val | Gly | Val | Pro | Gly | Val | Tyr | Thr | Asn |
| | | | | | 130 | | 135 | | | | | | | 140 | |
| Leu | Cys | Lys | Phe | Thr | Glu | Trp | Ile | Glu | Lys | Thr | Val | Gln | Ala | Ser | |
| | | | | | 145 | | | 150 | | | | | | 155 | |

(2) INFORMATION FOR SEQ ID NO:173:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1265 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:173:

| | | | | | | |
|------------|-------------|------------|------------|-------------|------------|-----|
| GGCAGCCCGC | ACTCGCAGGCC | CTGGCAGGCG | GCACTGGTCA | TGGAAAAACGA | ATTGTTCTGC | 60 |
| TCGGGCGTCC | TGGTGATCC | GCAGTGGGTG | CTGTGAGCCG | CACACTGTTT | CCAGAACTCC | 120 |
| TACACCATCG | GGCTGGGCCT | GCACAGTCTT | GAGGCCGACC | AAGAGCCAGG | GAGCCAGATG | 180 |
| GTGGAGGCCA | GCCTCTCCGT | ACGGCACCCA | GAGTACAACA | GACCCCTTGCT | CGCTAACGAC | 240 |

| | |
|---|------|
| CTCATGCTCA TCAAGTTGGA CGAATCCGTG TCCGAGTCTG ACACCACCG GAGCATTAGC | 300 |
| ATTGCTTCGC ACTGCCCTAC CGCGGGGAAAC TCTTGCTCTG TTTCCTGGCTG GGGTCTGCTG | 360 |
| CGGAACGGTG AGCTCACGGG TGTTGCTCTG CCCTCTTCAA GGAGGTCTC TGCCCGTGTG | 420 |
| CGGGGGCTGA CCCAGAGCTC TGCGTCCCAG GCAGAAATGCC TACCGTGTG CAGTGCCTGA | 480 |
| ACGTGTCGGT GGTGTCAGAG GAGGTCTGCA GTAAGCTCTA TGACCCGCTG TACCACCCCA | 540 |
| GCATGTTCTG CGCCGGCGGA GGGCAAGACC AGAAGGACTC CTGCAACGGT GACTCTGGGG | 600 |
| GGCCCCGTAT CTGCAACGGG TACTTGCAAGG GCCTTGTC TTTGGAAAAA GCCCGTGTG | 660 |
| GCCAAGTTGG CGTGCAGG GTCTACACCA ACCTCTGCAA ATTCACTGAG TGATAGAGA | 720 |
| AAACCGTCCA GGCCAGTTAA CTCTGGGAC TGGGAAACCA TGAAATTGAC CCCCAAATAC | 780 |
| ATCCTGCGGA AGGAATTCAAG GAATATCTGT TCCCAGCCCC TCCTCCCTCA GGCCAGGAG | 840 |
| TCCAGGCCCC CAGCCCTCC TCCCTCAAC CAAGGGTACA GATCCCCAGC CCTCTCTCCC | 900 |
| TCAGACCCAG GAGTCAGAC CCCCCAGCCC CTCCCTCTC AGACCCAGGA GTCCAGCCCC | 960 |
| TCCTCCNTCA GACCCAGGAG TCCAGACCCCC CCAGCCCCCTC CTCCCTCAGA CCCAGGGGTT | 1020 |
| GAGGGCCCCCA ACCCTCTCCTC CTTCAGAGTC AGAGGTCCAA GCCCCAACCC CCTCGTTCCC | 1080 |
| CAGACCCAGA GTGNNAAGGTC CCAGCCCCCTC TTCCNTCAGA CCCAGGGTC CAATGCCACC | 1140 |
| TAGATTTCTC CTGNACACAG TGCCCCCTTG TGGNANGTTG ACCCAACCTT ACCAGTTGGT | 1200 |
| TTTCATTTT TNGTCCCTT CCCCTAGATC CAGAAATAAA GTTTAAGAGA NGNGCAAAAAA | 1260 |
| AAAAAA | 1265 |

(2) INFORMATION FOR SEQ ID NO:174:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1459 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:174:

| | |
|--|------|
| GGTCAGCCGC ACACGTTTTC CAGAAAGTGA TGCAAGAGCTC CTACACCACATC GGGCTGGGCC | 60 |
| TGCACAGTCT TGAGGCCGAC CAAGAGCCAG GGAGCCAGAT GGTGGAGGCC AGCCTCTCCG | 120 |
| TACGGCACCC AGAGTACAAC AGACCTTGC TCGCTAACGA CCTCATGCTC ATCAAGTTGG | 180 |
| ACGAATCCGT GTCCGAGTCT GACACCATCC GGAGCATCAG CATTGCTTCG CAGTGCCCTA | 240 |
| CCGGGGGAA CTCTGCCCTC GTTTCTGGCT GGGGTCTGCT GGCAGACGGT GAGCTCACGG | 300 |
| GTGTGTGCTC GCCCCTCTCA AGGAGGTCT CTGCCAGTC GCAGGGGCTG ACCCAGAGCT | 360 |
| CTGCGTCCCA GGCAGAATGC CTACCGTGT GCAGTGCAG AAGCTGTCGG TGGTGTCTGA | 420 |
| NGAGGTCTGC ANTAAGCTCT ATGACCCGCT GTACCAACCC ANCATGTTCT GCGCCGGCG | 480 |
| AGGGCAAGAC CAGAAGGACT CCTGCAACGT GAGAGAGGGG AAAGGGGAGG GCAGGGCAGT | 540 |
| CAGGGAAGGG TGGAGAAGGG GGAGACAGAG ACACACAGGG CCGCATGGCG AGATGCAGAG | 600 |
| ATGGAGAGAC ACACAGGGAG ACAGTGACAA CTAGAGAGAG AAATGAGAG AACAGAGAA | 660 |
| ATAAACACAG GAATAAAGAG AAGCAAAAGG AGAGAGAAC AGAACACAGAC ATGGGGAGGC | 720 |
| AGAAACACAC ACACATAGAG ATGCAGTTGA CTTCCAACA GCATGGGGCC TGAGGGCGGT | 780 |
| GACCTCCACC CAATAGAAAA TTCTCTTATA ACTTTGACT CCCAAAAAAC CTGACTAGAA | 840 |
| ATAGCCTACT GTTGACGGG AGCCTTACCA ATAACATAAA TAGTCGATTT ATGCATACGT | 900 |
| TTTATGATT CATGATATAC CTTTGTGGAA ATTTTTGAT ATTTCTAACG TACACAGTTC | 960 |
| GTCTGTGAAT TTTTTAAAT TGTTGCACT CTCTAAAAT TTTCTGATG TGTTTATTGA | 1020 |
| AAAAATCCAA GTATAAGTGG ACTTGTGCAT TCAAACCAGG GTTGTCAAG GGTCAACTGT | 1080 |
| GTACCCAGAG GGAAACAGTG ACACAGATTC ATAGAGGTGA AACACGAAGA GAAACAGGAA | 1140 |
| AAATCAAGAC TCTACAAAGA GGCTGGGCAG GGTGGCTCAT GCCTGTAATC CCAGCACTTT | 1200 |
| GGGAGGCGAG GCAGGCAGAT CACTTGAGGT AAGGAGTTCA AGACCAGCCT GGCACAAATG | 1260 |
| GTGAAATCCT GTCTGTACTA AAAATACAAA AGTTAGCTGG ATATGGTGGC AGGCGCCTGT | 1320 |
| AATCCCAAGCT ACTTGGGAGG CTGAGGCAGG AGAATTGCTT GAATATGGGA GGCAGAGGTT | 1380 |
| GAAGTGAGTT GAGATCACAC CACTATACTC CAGCTGGGC AACAGAGTAA GACTCTGTCT | 1440 |
| CAAAAAAAAAA AAAAAAAAAA | 1459 |

(2) INFORMATION FOR SEQ ID NO:175:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1167 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Homo sapiens*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:175:

| | | | | | | |
|-------------|-------------|-------------|-------------|-------------|-------------|------|
| GCGCAGGCCCT | GGCAGGGCGGC | ACTGGTCATG | GAAAACGAAT | TGTTCTGCTC | GGGCGTCCCTG | 60 |
| GTGCATCCGC | AGTGGGTGCT | GTCAGCCGCA | CACTGTTCC | AGAACTCCCTA | CACCATCGGG | 120 |
| CTGGGCCTGC | ACAGTCTTGA | GGCCGACCAA | GAGCCAGGG | GCCAGATGGT | GGAGGCCAGC | 180 |
| CTCTCCGTAC | GGCACCCAGA | GTACAACAGA | CTCTTGCTCG | CTAACGACCT | CATGCTCATC | 240 |
| AAGTGGACG | AATCCGTGTC | CGAGCTGAC | ACCACATCCGA | GCATCAGCAT | TGCTTCGCAG | 300 |
| TGCCCTACCG | CGGGGAACTC | TTGGCTCGTN | TCTGGCTGGG | GTCCTGCTGGC | GAACGGCAGA | 360 |
| ATGCCCTACCG | TGCTGCACTG | CGTGAACTG | TCGGGTGTG | CTGAGGANGT | CTGCAGTAAG | 420 |
| CTCTATGACC | CGCTGTACCA | CCCCAGCTG | TTCTGCGCCG | GCGGAGGGCA | AGACCAAGAAG | 480 |
| GACTCTGCA | ACGGTGACTC | TGGGGGGCCC | CTGATCTGCA | ACGGGTACTT | GCAGGGCCTT | 540 |
| GTGTCTTCG | GAAAAGCCCC | GTGTGGCAA | CTTGGCGTGC | CAGGTGCTCA | CACCAACCTC | 600 |
| TGCAATTCA | CTGAGTGGAT | AGAGAAAACC | GTCCAGNCCA | GTAACTCTG | GGGACTGGGA | 660 |
| ACCCATGAAA | TTGACCCCCA | AATAACATCCT | GCGGAANGAA | TTCAGGAATA | TCTGTTCCCA | 720 |
| GCCCCCTCTC | CCTCAGGGCC | AGGAGTCCAG | GCCCCCAGCC | CCTCCTCCCT | CAAACCAAGG | 780 |
| GTACAGATCC | CCAGCCCCTC | CTCCCTCAGA | CCCAGGAGTC | CAGACCCCCC | AGCCCCCTCNT | 840 |
| CCNTCAGACC | CAGGAGTCCA | GCCCCCTCTC | CNTCAGACCC | AGGAGTCCAG | ACCCCCCAGC | 900 |
| CCNTCNCCTG | TCAGACCCAG | GGGTGCAAGC | CCCCAAGCCC | TCTCCNTCA | GAGTCAGAGG | 960 |
| TCCAAGCCCC | CAACCCCCCTG | TTCCCCCAGAC | CGAGAGGTNC | AGGTCCCGAC | CCCTCCTCC | 1020 |
| TCAGACCCAG | CGGTCTCACTG | CCACCTTAGAN | TNTCCCTGTA | CACAGTGGCC | CCTTGTGGCA | 1080 |
| NGTTGACCCA | ACCTTACAG | TTGGTTTTTC | ATTTTTTGTC | CCTTTCCCT | AGATCCAGAA | 1140 |
| ATAAAAGTNTA | AGAGAAAGGG | AAAAAAA | | | | 1167 |

(2) INFORMATION FOR SEQ ID NO:176:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 205 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Homo sapiens*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:176:

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Glu | Asn | Glu | Leu | Phe | Cys | Ser | Gly | Val | Leu | Val | His | Pro | Gln | Trp |
| 1 | | | | 5 | | | | | 10 | | | | | 15 | |

Val Leu Ser Ala Ala His Cys Phe Gln Asn Ser Tyr Thr Ile Gly Leu
 20 25 30

Gly Leu His Ser Leu Glu Ala Asp Gln Glu Pro Gly Ser Gln Met Val
35 40 45

Glu Ala Ser Leu Ser Val Arg His Pro Glu Tyr Asn Arg Leu Leu Leu
50 55 60

Ala Asn Asp Leu Met Leu Ile Lys Leu Asp Glu Ser Val Ser Glu Ser
 65 70 75 80

Asp Thr Ile Arg Ser Ile Ser Ile Ala Ser Gln Cys Pro Thr Ala Gly
 85 90 95

Asn Ser Cys Leu Val Ser Gly Trp Gly Leu Leu Ala Asn Gly Arg Met
 100 105 110

Pro Thr Val Leu His Cys Val Asn Val Ser Val Val Ser Glu Xaa Val
 115 120 125

Cys Ser Lys Leu Tyr Asp Pro Leu Tyr His Pro Ser Met Phe Cys Ala
 130 135 140

Gly Gly Gly Gln Asp Gln Lys Asp Ser Cys Asn Gly Asp Ser Gly Gly
 145 150 155 160

Pro Leu Ile Cys Asn Gly Tyr Leu Gln Gly Leu Val Ser Phe Gly Lys
 165 170 175

Ala Pro Cys Gly Gln Leu Gly Val Pro Gly Val Tyr Thr Asn Leu Cys
 180 185 190

Lys Phe Thr Glu Trp Ile Glu Lys Thr Val Gln Xaa Ser
 195 200 205

(2) INFORMATION FOR SEQ ID NO:177:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1119 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:177:

| | | | | | | |
|-------------|------------|------------|-------------|-------------|------------|------|
| GCGCACTCGC | AGCCCTGGCA | GGCGGCACGT | GTCATGGAAA | ACGAATTGTT | CTGCTGGGC | 60 |
| GTCCCTGGTC | ATCCGCACTG | GGTGCTGTCA | GCCGCACACT | GTTCCAGAA | CTCCTACACC | 120 |
| ATCGGGCTGG | GCCTGCACAG | TCTTGAGGCC | GACCAAGAGC | CAGGGAGCCA | GATGGTGGAG | 180 |
| GCCAGCCTCT | CCGTGACGCC | CCCAGAGTAC | AACAGACCCCT | TGCTCGCTAA | CGACCTCATG | 240 |
| CTCATCAAGT | TGGACGAATC | CGTGTCCGAG | TCTGACACCA | TCCGGAGCAT | CAGCATTGCT | 300 |
| TCGCACTGCC | CTACCGCGGG | GAACCTTGTG | CTCGTTCTG | GCTGGGGTCT | GCTGGCGAAC | 360 |
| GATGCTGTGA | TTGCCATCCA | GTCCCAGACT | GTGGGAGGCT | GGGAGTGTGA | GAAGCTTCC | 420 |
| CAACCCCTGGC | AGGGTTGTAC | CATTTGGCA | ACTTCCAGTG | CAAGGACGTC | CTGCTGCATC | 480 |
| CTCACTGGGT | GCTCACTACT | GCTCACTGCA | TCACCCGGAA | CACTGTGATC | AACTAGCCAG | 540 |
| CACCATAGTT | CTCCGAAGTC | AGACTATCAT | GATTACTGTG | TTGACTGTGC | TGTCTATTGT | 600 |
| ACTAACCATG | CCGATGTTTA | GGTAAATTAA | GCGTCACTTG | GCCTCAACCA | TCTTGGTATC | 660 |
| CAGTTATCCT | CACTGAATTG | AGATTTCTG | CTTCAGTGTC | AGCCATTCCC | ACATAATTTC | 720 |
| TGACCTACAG | AGGTGAGGGA | TCATATACT | CTTCAGGAT | GCTGGTACTC | CCCTCACAAA | 780 |
| TTCATTCTC | CTGTTGTAGT | GAAAGGTGCG | CCCTCTGGAG | CCTCCCAAGGG | TGGGTGTGCA | 840 |
| GGTCACAATG | ATGAATGTAT | GATCGTGTTC | CCATTACCCA | AAGCCTTAA | ATCCCTCATG | 900 |
| CTCACTACAC | CAGGGCAGGT | CTAGCATTTG | TTCATTAGT | GTATGCTGTC | CATTGATGCA | 960 |
| ACCACCTCAG | GACTCCTGGA | TTCTCTGCCT | AGTTGAGCTC | CTGCATGCTG | CCTCCTGGG | 1020 |
| GAGGTGAGGG | AGAGGGCCCA | TGGTTCAATG | GGATCTGTGC | AGTTGTAACA | CATTAGGTGC | 1080 |

TTAATAAACAA GAAGCTGTGA TGTTAAAAAA AAAAAAAA

1119

(2) INFORMATION FOR SEQ ID NO:178:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 164 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:178:

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Glu | Asn | Glu | Leu | Phe | Cys | Ser | Gly | Val | Leu | Val | His | Pro | Gln | Trp |
| 1 | | | | 5 | | | | | 10 | | | | 15 | | |
| Val | Leu | Ser | Ala | Ala | His | Cys | Phe | Gln | Asn | Ser | Tyr | Thr | Ile | Gly | Leu |
| | 20 | | | | | | 25 | | | | | 30 | | | |
| Gly | Leu | His | Ser | Leu | Glu | Ala | Asp | Gln | Glu | Pro | Gly | Ser | Gln | Met | Val |
| | 35 | | | | | 40 | | | | | 45 | | | | |
| Glu | Ala | Ser | Leu | Ser | Val | Arg | His | Pro | Glu | Tyr | Asn | Arg | Pro | Leu | Leu |
| | 50 | | | | | 55 | | | | | 60 | | | | |
| Ala | Asn | Asp | Leu | Met | Leu | Ile | Lys | Leu | Asp | Glu | Ser | Val | Ser | Glu | Ser |
| | 65 | | | | | 70 | | | | | 75 | | | 80 | |
| Asp | Thr | Ile | Arg | Ser | Ile | Ser | Ile | Ala | Ser | Gln | Cys | Pro | Thr | Ala | Gly |
| | | 85 | | | | | 90 | | | | | | 95 | | |
| Asn | Ser | Cys | Leu | Val | Ser | Gly | Trp | Gly | Leu | Leu | Ala | Asn | Asp | Ala | Val |
| | | | 100 | | | | 105 | | | | | 110 | | | |
| Ile | Ala | Ile | Gln | Ser | Xaa | Thr | Val | Gly | Gly | Trp | Glu | Cys | Glu | Lys | Leu |
| | | | 115 | |) | | 120 | | | | 125 | | | | |
| Ser | Gln | Pro | Trp | Gln | Gly | Cys | Thr | Ile | Ser | Ala | Thr | Ser | Ser | Ala | Arg |
| | | 130 | | | | 135 | | | | | 140 | | | | |
| Thr | Ser | Cys | Cys | Ile | Leu | Thr | Gly | Cys | Ser | Leu | Leu | Leu | Thr | Ala | Ser |
| | 145 | | | | 150 | | | | | 155 | | | 160 | | |
| Pro | Gly | Thr | Leu | | | | | | | | | | | | |

(2) INFORMATION FOR SEQ ID NO:179:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 250 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:179:

CTGGAGTGCC TTGGTGTTC AAGCCCTGC AGGAAGCAGA ATGCACCTTC TGAGGCACCT 60

| | | | | | | |
|------------|------------|------------|------------|------------|-------------|-----|
| CCAGCTGCC | CCGGCCGGGG | GATGCGAGGC | TGGAGCAC | CTTGGCCGGC | TGTGATTGCT | 120 |
| GCCAGGC | ACT | GTTCATCTCA | GCTTTCTGT | CCCTTGCTC | CCGGCAAGCG | 180 |
| AAGTTCATAT | CTGGAGCCTG | ATGTCTAAC | GAATAAAGGT | CCCATGCTCC | ACCCGAAAAAA | 240 |
| AAAAAAAAAA | | | | | | 250 |

(2) INFORMATION FOR SEQ ID NO:180:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 202 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:180:

| | | | | | | |
|------------|-------------|------------|------------|------------|------------|-----|
| ACTAGTCCAG | TGTGGTGGAA | TTCCATTGTG | TTGGGCCAA | CACAATGGCT | ACCTTTAAC | 60 |
| TCACCCAGAC | CCCGCCCCCTG | CCCGTCCCC | ACGCTGCTGC | TAACGACAGT | ATGATGCTTA | 120 |
| CTCTGCTACT | CGAAACTAT | TTTTATGTAA | TTAATGTATG | CTTTCTTGT | TATAAATGCC | 180 |
| TGATTAAAAA | AAAAAAA | AA | | | | 202 |

(2) INFORMATION FOR SEQ ID NO:181:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 558 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:181:

| | | | | | | |
|------------|-------------|-------------|------------|------------|-------------|-----|
| TCCYTTTGKT | NAGGTTKKKG | AGACAMCCCK | AGACCTWAAN | CTGTGTCACA | GACTTCYNGG | 60 |
| AATGTTTAGG | CAGTGCTAGT | AATTTCYTCG | TAATGATTCT | GTTATTACTT | TCCTNATTCT | 120 |
| TTATTCTCT | TTCTTCTGAA | GATTAATGAA | GTTGAAAATT | GAGGTGGATA | AATACAAAAAA | 180 |
| GGTAGTGTGA | TAGTATAAGT | ATCTAAGTGC | AGATGAAAGT | GTGTTATATA | TATCCATTCA | 240 |
| AAATTATGCA | AGTTAGTAAAT | TACTCAGGGT | TAACTAAATT | ACTTTAATAT | GCTGTTGAAC | 300 |
| CTACTCTGTT | CCTTGGCTAG | AAAAAAATTAT | AAACAGGACT | TTGTTAGTTT | GGGAAGGCCAA | 360 |
| ATTGATAATA | TTCTATGTT | AAAAAGTTGG | GCTATACATA | AATTATTAAG | AAATATGGAW | 420 |
| TTTTATTCCC | AGGAATATGG | KGTTCACTTT | ATGAATATTA | CSCRGGATAG | AWGTWTGAGT | 480 |
| AAAAYCAGTT | TTGGTWAATA | YGTWAATATG | TCMTAAATAA | ACAAKGTTT | GACTTATTTC | 540 |
| CAAAAAAAA | AAAAAAA | | | | | 558 |

(2) INFORMATION FOR SEQ ID NO:182:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 479 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:182:

| | | | | | | |
|------------|-------------|-------------|-------------|-------------|------------|-----|
| ACAGGGWTK | GRGGATGCTA | AGSCCCCRGA | RWTYGTGTTGA | TCCAACCCCTG | GCTTWTTTTC | 60 |
| AGAGGGAAA | ATGGGGCCCTA | GAAGTTACAG | MSCATYTAGY | TGGTGCGMTG | GCACCCCTGG | 120 |
| CSTCACACAG | ASTCCCCAGT | AGCTGGGACT | ACAGGCACAC | AGTCACTGAA | GCAGGCCCTG | 180 |
| TTWGCAATT | ACGTTGCCAC | CTCCAACCTTA | AACATTCTTC | ATATGTGATG | TCTTAGTCA | 240 |
| CTAAGGITAA | ACTTCCCAC | CCAGAAAAGG | CAACTTAGAT | AAAATCTTAG | AGTACTTTCA | 300 |
| TACTMTTCTA | AGTCCTCTTC | CAGCCTCACT | KKGAGTCCTM | CYTGGGGTT | GATAGGAANT | 360 |
| NTCTCTTGGC | TTTCTCAATA | AARTCTCTAT | YCATCTCATG | TTAATTGG | TACGCATARA | 420 |

AWTGSTGARA AAATTAAAAT GTTCTGGTTY MACTTTAAAA ARAAAAAAAA AAAAAAAA 479

(2) INFORMATION FOR SEQ ID NO:183:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 384 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:183:

| | |
|---|-----|
| AGGCGGGAGC AGAACGCTAA | 60 |
| GCCAAAGCCC AAGAACAGTG | 120 |
| GCAGTGCCAG CACTGGTGCC | 180 |
| AGTACCAAGTA CCAATAACAG TGCCAGTGCC AGTGCAGCA CCAGTGGTGG CTTCACTGCT | 240 |
| GGTGCAGGCC TGACCGCCAC TCTCACATT GGGCTCTCG CTGGCCTTGG TGGAGCTGGT | 300 |
| GCCAGCACCA GTGCGAGCTC TGGTGCCTGT GGTTTCCTT ACAAGTGAGA TTTTAGATAT | 360 |
| TGTTAACCTCT GCCAGTCTTT CTCTTCAGC CAGGGCAT CCTCAGAAC CTACTCAACA | 384 |
| CAGCACTCTA GCGAGCCACT ATCAATCAAT TGAAGTTGAC ACTCTGCATT ARATCTATTT | |
| GCCATTCAA AAAAAAAA AAAA | |

(2) INFORMATION FOR SEQ ID NO:184:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 496 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:184:

| | |
|---|-----|
| ACCGAATTGG GACCCTGGC TTATAAGCGA TCATGTYNT CCRGTTATKAC CTCAACGAGC | 60 |
| AGGGAGATCG AGTCTATACG CTGAAGAAAT TTGACCCAT GGGACAACAG ACCTGCTCAG | 120 |
| CCCATCCTGC TCGGTTCTCC CCAGATGACA AATACTCTSG ACACCGAATC ACCATCAAGA | 180 |
| AACCTTCAA GGTGCTCATG ACCCAGCAAC CGCGCCCTGT CCTCTGAGGG TCCCTTAAAC | 240 |
| TGATGCTTT TCTGCCACCT GTTACCCCTC GGAGACTCCG TAACCAAACCT TTTCGGACTG | 300 |
| TGAGCCCTGA TGCCTTTTG CCAGCCATAC TCTTGGCAT CCAGTCTCTC GTGGCGATTG | 360 |
| ATTATGCTTG TGTGAGGCAA TCATGGTGGC ATCACCCATA AAGGGAACAC ATTTGACTTT | 420 |
| TTTTTCTCAT ATTTAAATT ACTACMAGAW TATTWMAW WAAATGAWTT GAAAAACTST | 480 |
| AAAAAAAAAA AAAA | 496 |

(2) INFORMATION FOR SEQ ID NO:185:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 384 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:185:

| | |
|---|-----|
| GCTGGTAGCC TATGGCGKGG CCCACGGAGG GGCTCCTGAG GCCACGGRAC AGTGAATTCC | 60 |
| CAAGTATCYT GCGCSGCGTC TTCTACCGTC CCTACCTGCA GATCTTCGGG CAGATTCCCC | 120 |
| AGGAGGACAT GGACGTGGCC CTCATGGAGC ACAGCAACTG YTCTGCGGAG CCCGGCTTCT | 180 |
| GGGCACACCC TCCTGGGGCC CAGGCAGGCA CCTGCGTCTC CCAGTATGCC AACTGGCTGG | 240 |
| TGGTGCCTGCT CCTCGTCATC TTCTGCTCG TGGCCAACAT CCTGCTGGTC AACTTGCTCA | 300 |
| TTGCCATGTT CAGTTACACA TTCGGCAAAG TACAGGGCAA CAGGGATCTC TACTGGGAAG | 360 |
| GCGCAGCGTT ACCGCCTCAT CCGG | 384 |

(2) INFORMATION FOR SEQ ID NO:186:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 577 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:186:

| | | | | | | |
|-------------|-------------|-------------|-------------|--------------|-------------|-----|
| GAGTTAGCTC | CTCCACAAACC | TTGATGAGGT | CGTCTGCAGT | GGCCTCTCGC | TTCATACCGC | 60 |
| TNCATCGTC | ATACTGTAGG | TTTGCCACCA | CYTCTGGCA | TCTTGGGCG | GCNTAATATT | 120 |
| CCAGGAAACT | CTCAATCAAG | TCACCGTCGA | TGAAACCTGT | GGGCTGGTTC | TGTCTTCGC | 180 |
| TCGGTGTGAA | AGGATCTCCC | AGAAGGAGTC | CTCGATCTTC | CCCACACTTT | TGATGACTTT | 240 |
| ATTGAGTCGA | TTCTGCATGT | CCAGCAGGAG | GTTGTACCGAG | CTCTCTGACA | GTGAGGTAC | 300 |
| CAGCCCTATC | ATGCCGTGAA | MCGTGCAGA | GARCAACCGAG | CCTTGTGTGG | GGGKKGAAGT | 360 |
| CTCACCCAGA | TTCTGCATTA | CCAGAGAGCC | GTGGCAAAG | ACATTGACAA | ACTCGCCCCAG | 420 |
| GTGAAAAAAAG | AMCAMCTCCT | GGARGTGCCTN | GGCGCTCCTC | GTCMGTGTTGGT | GGCAGCGCTW | 480 |
| TCTTTTGAC | ACACAAACAA | GTTAAAGGCA | TTTCAGCCC | CCAGAAANTT | GTCATCATCC | 540 |
| AAGATNTCGC | ACAGCACTNA | TCCAGTTGGG | ATTAAAT | | | 577 |

(2) INFORMATION FOR SEQ ID NO:187:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 534 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:187:

| | | | | | | |
|-------------|-------------|------------|-------------|-------------|------------|-----|
| AACATCTTCC | TGTATAATGC | TGTGTAATAT | CGATCCGATN | TTGTCGTGSTG | AGAATYCATW | 60 |
| ACTKGAAAAA | GMAACATTAA | AGCCTGGACA | CTGGTATTAA | AATTACAAT | ATGCAACACT | 120 |
| TTAACACGTG | TGTCAATCTG | CTCCCYYNAC | TTTGTCACTCA | CCAGTCTGGG | AAKAAGGGTA | 180 |
| TGCCCTATTCA | ACACCTGTTA | AAAGGGCGCT | AAGCATTTTT | GATTCAACAT | CTTTTTTTT | 240 |
| GACACAAGTC | CGAAAAAAAGC | AAAAGTAAAC | AGTTATYATAT | TTGTTAGCCA | ATTCACTTTC | 300 |
| TTCATGGGAC | AGAGCCATYT | GATTTAAAAA | GCAAATTGCA | TAATATTGAG | CTTYGGGAGC | 360 |
| TGATATTGAG | GCGGAAGAGT | AGCCTTCTA | CTTCACCCAGA | CACAACCTCCC | TTTCATATTG | 420 |
| GGATGTTNAC | NAAAGTWATG | TCTCTWACAG | ATGGGATGCT | TTTGTGGCAA | TTCTGTTCTG | 480 |
| AGGATCTCCC | AGTTTATTAA | CCACTTGCAC | AAGAAGGCGT | TTTCTTCCTC | AGGC | 534 |

(2) INFORMATION FOR SEQ ID NO:188:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 761 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:188:

| | | | | | | |
|------------|------------|------------|------------|-------------|------------|-----|
| AGAAACCAGT | ATCTCTAAA | ACAACCTCTC | ATACCTTGTG | GACCTAATTT | TGTGTGCGTG | 60 |
| TGTGTGTGCG | CGCATATTAT | ATAGACAGGC | ACATCTTTT | TACTTTTGTA | AAAGCTTATG | 120 |
| CCTCTTTGGT | ATCTATATCT | GTGAAAGTTT | TAATGATCTG | CCATAATGTC | TTGGGGACCT | 180 |
| TTGTCTTCTG | TGTAAATGGT | ACTAGAGAAA | ACACCTATNT | TATGAGTCAA | TCTAGTTNGT | 240 |
| TTTATTGAC | ATGAAGGAAA | TTTCCAGATN | ACAACACTNA | CAAACCTCTCC | CTKGACKARG | 300 |
| GGGGACAAAG | AAAAGCAAAA | CTGAMCATAA | RAAACATWA | CCTGGTGAGA | ARTTGCATAA | 360 |
| ACAGAAATWR | GGTAGTATAT | TGAARNACAG | CATCATTAAA | RMGTTWTKTT | WTCTCCCTT | 420 |

| | | | | | | |
|-----------------------|------------|------------|------------|------------|------------|-----|
| GCAAAAAACA TGTACNGACT | TCCCGTTGAG | TAATGCCAAG | TTGTTTTTT | TATNATAAAA | 480 | |
| CTTGCCTTC | ATTACATGTT | TNAAGTGGT | GTGGTGGGCC | AAAATATTGA | AATGATGGAA | 540 |
| CTGACTGATA | AAGCTGTACA | ATAAAGCAGT | GTGCCAACAA | AGCAACACAG | TAATGTTGAC | 600 |
| ATGCTTAATT | CACAAATGCT | AATTCTATTA | TAATGTTTG | CTAAAATACA | CTTGTAACTA | 660 |
| TTTTCTGTN | TTCCCAGAGC | TGAGATNTA | GATTTATGT | AGTATNAAGT | GAAAANTAC | 720 |
| GAAAATAATA | ACATTGAAGA | AAAANANAAA | AAANAAAAAA | A | | 761 |

(2) INFORMATION FOR SEQ ID NO:189:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 482 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:189:

| | | | | | | |
|------------|-------------|------------|------------|------------|-------------|-----|
| TTTTTTTTT | TTTGCGATN | CTACTATTTT | ATTGCAGGAN | GTGGGGGTGT | ATGCACCGCA | 60 |
| CACCGGGGCT | ATNAGAAGCA | AGAAGGAAGG | AGGGAGGGCA | CAGCCCCCTG | CTGAGCAAACA | 120 |
| AAGCCCCCTG | CTGCCCTCTC | TGTCTGTCTC | CTGGTGCAGG | CACATGGGA | GACCTTCCCC | 180 |
| AAGGCAGGGG | CCACCAAGTCC | AGGGGTGGGA | ATACAGGGGG | TGGGANGTGT | GCATAAGAAG | 240 |
| TGATAGGCAC | AGGCCACCCG | GTACAGACCC | CTCGGCTCCT | GACAGGTNGA | TTTCGACCAAG | 300 |
| GTCATTGTGC | CCTGCCAGG | CACAGCGTAN | ATCTGGAAA | GACAGAATGC | TTTCCTTTTC | 360 |
| AAATTTGGCT | NGTCATNGAA | NGGCANTTT | TCCAANTTNG | GCTNGGTCTT | GGTACNCTTG | 420 |
| GTCAGGCCA | GCTCCNCCTC | CAAAAANTAT | TCACCCNNCT | CCNAATTGCT | TGCNGGNCCC | 480 |
| CC | | | | | | 482 |

(2) INFORMATION FOR SEQ ID NO:190:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 471 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:190:

| | | | | | | |
|-------------|------------|-------------|------------|------------|-------------|-----|
| TTTTTTTTT | TTTTAAAACA | GTTTTCACCA | ACAAAATTAA | TTAGAAGAAT | AGTGGTTTG | 60 |
| AAAACCTCTG | CATCCAGTGA | GAACATACCAT | ACACACATT | ACAGCTNGGA | ATGTNCTCCA | 120 |
| AATGTCCTGGT | CAAATGATAC | AATGGAACCA | TTCAATCTTA | CACATGCAGG | AAAGAACAAAG | 180 |
| CGCTTTGAC | ATACAATGCA | CAAAAAAAA | AGGGGGGGGG | GACCACATGG | ATTTAAATTT | 240 |
| TAAGTACTCA | TCACATACAT | TAAGACACAG | TTCTAGTCCA | GTCNAAAATC | AGAACTGCNT | 300 |
| TGAAAAAATTT | CATGTATGCA | ATCCAACCAA | AGAACTTNAT | TGGTGATCAT | GANTNCTCTA | 360 |
| CTACATCNAC | CTTGATCATT | GCCAGGAACN | AAAAGTTNA | ANCACNCNGT | ACAAAAANAA | 420 |
| TCTGTAATTN | ANTTCAACCT | CCGTACNGAA | AAATNTNNNT | TATACACTCC | C | 471 |

(2) INFORMATION FOR SEQ ID NO:191:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 402 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:191:

| | | | | | | |
|------------|------------|------------|-------------|------------|------------|-----|
| GAGGGATTGA | AGGTCTGTTC | TASTGTCGGM | CTGTTCAAGCC | ACCAACTCTA | ACAAGTTGCT | 60 |
| GTCTTCCACT | CACTGTCTGT | AAGCTTTTA | ACCCAGACWG | TATCTTCATA | AATAGAACAA | 120 |

| | |
|--|-----|
| ATTCTTCACC AGTCACATCT TCTAGGACCT TTTGGATTC ACTTAGTATA AGCTCTCCA | 180 |
| CTTCCTTGT TAAGACTTCA TCTGGTAAAG TCTTAAGTTT TGTAGAAAGG AATTYAATTG | 240 |
| CTCGTCTCT AACAAATGTCC TCTCCTGAA GTATTTGGCT GAACAACCCA CCTAAAGTCC | 300 |
| CTTGTGCAT CCATTTAAA TATACTTAAT AGGSCATTGK TNCACTAGGT TAAATTCTGC | 360 |
| AAGAGTCATC TGTCTGCAA AGTTGCGTTA GTATATCTGC CA | 402 |

(2) INFORMATION FOR SEQ ID NO:192:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 601 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:192:

| | |
|--|-----|
| GAGCTCGGAT CCAATAATCT TTGTCTGAGG GCAGCACACA TATNCAGTGC CATGGNAACT | 60 |
| GGTCTACCCC ACATGGGAGC AGCATGCCGT AGNTATATAA GGTCAATTCCC TGAGTCAGAC | 120 |
| ATGCYTYTTT GAYTACCGTG TGCCAAGTGC TGGTGATTCT YAACACACYT CCATCCCCYT | 180 |
| CTTTGTGGA AAAACTGGCA CTTKTCCTGA ACTAGCARGA CATCACTTAC AAATTCAACC | 240 |
| ACGAGACACT TGAAAGGTGT AACAAAGCGA YTCTTGCAATT GCTTTTGTC CCTCCGGCAC | 300 |
| CAGTTGTCAA TACTAACCCG CTGGTTGCC TCCATCACAT TTGTGATCTG TAGCTCTGGA | 360 |
| TACATCTCCT GACAGTACTG AAGAACATTCT TCTTTGTTT CAAAAGCARC TCTTGGTGCC | 420 |
| TGTTGGATCA GGTTCCATT TCCCACTCYG AATGTTACAA TGGCATATT WACTTCCAC | 480 |
| AAAACATTGC GATTGAGGC TCAGCAACAG CAAATCCTGT TCCGGCATG GCTGCAAGAG | 540 |
| CCTCGATGTA GCCGCCAGC GCCAAGGCAG GCGCCGTGAG CCCCACCCAGC AGCAGAAGCA | 600 |
| G | 601 |

(2) INFORMATION FOR SEQ ID NO:193:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 608 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:193:

| | |
|---|-----|
| ATACAGCCCA NATCCCACCA CGAAGATGCG CTTGTTGACT GAGAACCTGA TGCAGTCACT | 60 |
| GGTCCCGCTG TAGCCCCAGC GACTCTCCAC CTGCTGGAAG CGGTTGATGC TGCACCTCYTT | 120 |
| CCCAACGCG GCAGMAGCGG GSCCGGTCAA TGAACCTCCAY TCGTGGCTTG GGGTKGACGG | 180 |
| TKAAGTGCAG GAAGAGGCTG ACCACCTCGC GGTCCACCG GATGCCCCGAC TGTGCGGGAC | 240 |
| CTGCAGCGAA ACTCCTCGAT GGTCACTGAGC GGGAAAGCGAA TGAGGCCCCAG GGCCTTGCC | 300 |
| AGAACCTTCTC GCCTGTTCTC TGCGCTCACCG TGAGCTGCT GCGCTGACA CTCGGCTCG | 360 |
| GACCAGCGGA CAAACGGCRT TGAACAGCGG CACCTCACGG ATGCCCCAGTG TGTGCGCTC | 420 |
| CAGGAMMGS ACCAGCGTGT CCAGGTCAAT GTCGGTGAAG CCCTCCGCGG GTRATGGCGT | 480 |
| CTGCAGTGT TTTGTGATG TTCTCAGGC ACAGGCTGGC CAGCTGCGGT TCATCGAAGA | 540 |
| GTCGCGCTG CGTGAGCAGC ATGAAGGCAGT TGTGGCTCG CAGTTCTTCT TCAGGAACTC | 600 |
| CACGCAAT | 608 |

(2) INFORMATION FOR SEQ ID NO:194:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 392 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:194:

| | | | | | | |
|------------|------------|------------|------------|------------|-------------|-----|
| GAACGGCTGG | ACCTTGCCTC | GCATTGTGCT | TGCTGGCAGG | GAATACCTTG | GCAAGCAGYT | 60 |
| CCAGTCGAG | CAGCCCCAGA | CCGCTGCCGC | CCGAAGCTAA | GCCTGCCTCT | GGCCTTCCCC | 120 |
| TCCGCCTCAA | TGCAGAACCA | GTAGTGGAG | CACTGTGTTT | AGAGTTAAGA | GTAACACTG | 180 |
| TTTGATTTA | CTTGGGAATT | TCCTCTGTTA | TATAGCTTTT | CCCAATGCTA | ATTCCTCAAAC | 240 |
| AACAACAACA | AAATAACATG | TTTGCCTGTT | AAGTTGTATA | AAAGTAGGTG | ATTCTGTATT | 300 |
| TAAGAAAAT | ATTACTGTTA | CATACTGC | TTGCAATTTC | TGTATTATT | GKTNCTSTGG | 360 |
| AAATAAATAT | AGTTATTAAA | GGTTGTCANT | CC | | | 392 |

(2) INFORMATION FOR SEQ ID NO:195:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 502 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:195:

| | | | | | | |
|------------|--------------|------------|------------|-------------|------------|-----|
| CCSTTKGAGG | GGTKAGGKYC | CAGTTYCCGA | GTGGAAGAAA | CAGGCCAGGA | GAAGTGCCTG | 60 |
| CCGAGCTGAG | GCAGATGTTTC | CCACAGTGAC | CCCCAGAGCC | STGGGSTATA | GTYTCTGACC | 120 |
| CCTCNCAAGG | AAAGACCACCS | TTCTGGGAC | ATGGGCTGGA | GGGCAGGACC | TAGAGGCACC | 180 |
| AAGGGAAGGC | CCCATTCCCG | GGSTGTTCCC | CGAGGAGGAA | GGGAAGGGGC | TCTGTGTGCC | 240 |
| CCCCASGAGG | AAGAGGCCCT | GAGTCCTGGG | ATCAGACACC | CCTTCACGTG | TATCCCCACA | 300 |
| CAAATGCAAG | CTCACCAAGG | TCCCCTCTCA | GTCCCCCTCC | STACACCCCTG | AMCGGCCACT | 360 |
| GSCSCACACC | CACCCAGAGC | ACGCCACCCG | CCATGGGGAR | TGTGCTCAAG | GARTCGCNNG | 420 |
| GCARCGTGG | CATCTNGTCC | CAGAAGGGGG | CAGAATCTCC | AATAGANGGA | CTGARCMSTT | 480 |
| GCTNAAAAAA | AAAAAANAAAAA | AA | | | | 502 |

(2) INFORMATION FOR SEQ ID NO:196:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 665 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:196:

| | | | | | | |
|------------|------------|------------|------------|------------|------------|-----|
| GGTTACTTGG | TTTCATTGCC | ACCACTTAGT | GGATGTCATT | TAGAACCATT | TTGTCTGCTC | 60 |
| CCTCTGGAAG | CCTTGCAG | AGCGGACTTT | GTAATTGTTG | GAGAATAACT | GCTGAATTTT | 120 |
| WAGCTGTTK | GAGTTGATTG | GCACCACTGC | ACCCACAAC | TCAATATGAA | AACYAWTTGA | 180 |
| ACTWATTTAT | TATCTTGTA | AAAAGTAAAC | AATGAAAATT | TTGTTCATAC | TGTATTKATC | 240 |
| AAGTATGATG | AAAAGCAAWA | GATATATATT | CTTTTATTAT | GTAAATTAT | GATTGCCATT | 300 |
| ATTAATCGGC | AAAATGTGGA | GTGTATGTC | TTTCACAGT | AATATATGCC | TTTTGTAACT | 360 |
| TCACTTGGT | ATTTTATTGT | AAATGARTTA | CAAATTCTT | AATTTAAGAR | AATGGTATGT | 420 |
| WATATTATT | TCAATTATT | CTTTCCTKGT | TTACGTTAAT | TTGAAAAGA | WTGCATGATT | 480 |
| TCTTGACAGA | AATCGATCTT | GATGCTGTTG | AAGTAGTTG | ACCCACATCC | CTATGAGTTT | 540 |
| TTCTTGAAT | GTATAAAGGT | TGTAGCCCAT | CNAACCTCAA | AGAAAAAAAT | GACCACATAC | 600 |
| TTTGCAATCA | GGCTGAAATG | TGGCATGCTN | TTCTAATTCC | AACTTTATAA | ACTAGCAAAN | 660 |
| | AAGTG | | | | | 665 |

(2) INFORMATION FOR SEQ ID NO:197:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 492 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:197:

| | | | | | | |
|------------|------------|------------|------------|------------|------------|-----|
| TTTTNTTTTT | TTTTTTTG | AGGAAGGATT | CCATTATTG | TGGATGCATT | TTCACAATAT | 60 |
| ATGTTTATTG | GAGCGATCCA | TTATCAGTGA | AAAGTATCAA | GTGTTATAA | NATTTTAGG | 120 |
| AAGGCAGATT | CACAGAACAT | GCTNGCNGC | TTGCAGTTT | ACCTCGTANA | GATNACAGAG | 180 |
| AATTATAGTC | NAACCAGTAA | ACNAGGAATT | TACTTTCAA | AAGATTAAT | CCAAACTGAA | 240 |
| CAAAATTCTA | CCCTGAAACT | TACTCCATCC | AAATATTGGA | ATAANAGTCA | GCAGTGATAC | 300 |
| ATTCTCTTCT | GAACTTAGA | TTTCTAGAA | AAATATGAA | TAGTGATCG | GAAGAGCTCT | 360 |
| TGTTCAAAAG | TACAACNAAG | CAATGTTCC | TTACCATAGG | CCTTAATTCA | AACTTTGATC | 420 |
| CATITCACTC | CCATCACGGG | AGTCAATGCT | ACCTGGGACA | CTTGTATTT | GTTCATNCTG | 480 |
| ANCNTGGCTT | AA | | | | | 492 |

(2) INFORMATION FOR SEQ ID NO:198:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 478 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:198:

| | | | | | | |
|------------|-------------|------------|-------------|-------------|------------|-----|
| TTTNTTTTGN | ATTTCANCT | GTANNAANTA | TTTTCATTAT | GTATTATTANA | AAAATATNAA | 60 |
| TGTNTCCACN | ACAAATCATN | TTACNTNAGT | AAAGAGGCCAN | CTACATTGTA | CAACATACAC | 120 |
| TGAGTATATT | TTGAAAAAGGA | CAAGTTAAA | GTANACNCAT | ATTGCCGANC | ATANCACATT | 180 |
| TATACATGGC | TTGATTGATA | TTTAGCACAG | CANAAACTGA | GTGAGTTACC | AGAAANAAAT | 240 |
| NATATATGTC | AATCNGATT | AAGATACAAA | ACAGATCCTA | TGGTACATAN | CATCNTGTA | 300 |
| GAGTTGTGGC | TTTATGTTA | CTGAAAGTCA | ATGCAGTTCC | TGACAAAGA | GATGGCCGTA | 360 |
| AGCATTCTAG | TACCTCTACT | CCATGGTAA | GAATCGTACA | CTTATGTTA | CATATGTNCA | 420 |
| GGGTAAGAAT | TGTGTTAAGT | NAANTTATGG | AGAGGTCCAN | GAGAAAAATT | TGATNCAA | 478 |

(2) INFORMATION FOR SEQ ID NO:199:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 482 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:199:

| | | | | | | |
|------------|------------|------------|------------|------------|------------|-----|
| AGTGACTTGT | CCTCCAACAA | AACCCCTTGA | TCAAGTTGT | GGCACTGACA | ATCAGACCTA | 60 |
| TGCTAGTTCC | TGTCATCTAT | TCGCTACTAA | ATGCAGACTG | GAGGGACCA | AAAAGGGCA | 120 |
| TCAACTCCAG | CTGGATTATT | TTGGAGCCTG | CAAATCTATT | CCTACTTGTA | CGGACTTTGA | 180 |
| AGTGATTCA | TTTCCTCTAC | GGATGAGAGA | CTGGCTCAAG | AAATACCTCA | TGCAGCTTA | 240 |
| TGAAGCCNAC | TCTGAACACG | CTGCTTATCT | NAGATGAGAA | NCAGAGAAAT | AAAGTCNAGA | 300 |
| AAATTACCT | GGANGAAAAG | AGGCTTNGG | CTGGGGACCA | TCCCATTGAA | CCTTCTCTTA | 360 |
| ANGGACTTTA | AGAANAAAAT | ACCACATGTN | TGTNGTATCC | TGGTGCCNGG | CCGTTTANTG | 420 |
| AACNTNGACN | NCACCCCTNT | GGAATANANT | CTTGACNGCN | TCCTGAACCT | GCTCCTCTGC | 480 |
| GA | | | | | | 482 |

(2) INFORMATION FOR SEQ ID NO:200:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 270 base pairs
 - (B) TYPE: nucleic acid

- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:200:

| | | | | | | |
|------------|------------|------------|------------|-------------|------------|-----|
| CGGCCGCAAG | TGCAACTCCA | GCTGGGGCCC | TGCAGACGAA | GATTCTGCCA | GCAGTTGGTC | 60 |
| CGACTGCGAC | GACGGCGCCG | GCGACAGTCC | CAGGTGCAGC | GCGGGCGCCT | GGGGTCTTGC | 120 |
| AAGGCTGAGC | TGACGCCGCA | GAGGTCTGTG | CACGTCAC | GACCTTGACG | CCGTCGGGGA | 180 |
| CAGCCGGAAC | AGAGCCCGGT | GAANGCGGGA | GGCCTCGGGG | AGCCCCCTCGG | GAAGGGCGGC | 240 |
| CCGAGAGATA | CGCAGGTGCA | GGTGGCCGCC | | | | 270 |

(2) INFORMATION FOR SEQ ID NO:201:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 419 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:201:

| | | | | | | |
|------------|-------------|------------|------------|------------|-------------|-----|
| TTTTTTTTTT | TTTTGGAATC | TACTGGGAGC | ACAGCAGGTC | AGCAACAAGT | TTATTTGCA | 60 |
| GCTAGCAAGG | TAACAGGGTA | GGGCATGGTT | ACATGTTCA | GTCAACTTCC | TTTGTCTGG | 120 |
| TTGATTGGTT | TGTCTTATG | GGGGCGGGGT | GGGTAGGGG | AAANCGAAGC | ANAANTAAACA | 180 |
| TGGAGTGGGT | GCACCCCTCCC | TGTAGAACCT | GGTTACNAAA | GCTTGGGGCA | GTTCACCTGG | 240 |
| TCTGTGACCG | TCATTTCTT | GACATCAATG | TTATTAGAAG | TCAGGATATC | TTTAGAGAG | 300 |
| TCCACTGTNT | CTGGAGGGAG | ATTAGGGTTT | CTTGCCAANA | TCCAANAAA | ATCCACNTGA | 360 |
| AAAAGTTGGA | TGATNCANGT | ACNGAATACC | GANGGCATAN | TTCTCATANT | CGGTGGCCA | 419 |

(2) INFORMATION FOR SEQ ID NO:202:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 509 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:202:

| | | | | | | |
|------------|------------|------------|------------|-------------|-------------|-----|
| TTTTTTTTTT | TTTTTTTTTT | TTTTTTTTTT | TTTTTTTTTT | TTTTTTTTTT | TTTTTTTTTT | 60 |
| TGGCACTTAA | TCCATTTTA | TTTCAAAATG | TCTACAAANT | TTNAATNCNC | CATTATAACNG | 120 |
| GTNATTTCNC | AAAATCTAA | NNTTATTCAA | ATNTNAGCCA | AANTCCTTAC | NCAAATNNAA | 180 |
| TACCNCAAA | AATCAAAAT | ATACNTNTCT | TTCAGCAAC | TTNGTTACAT | AAATTAAAAA | 240 |
| AATATATACG | GCTGGTGT | TCAAAGTACA | ATTATCTAA | CACTGCAAC | ATNTTTNNAA | 300 |
| GGAACTAAAA | TAAAAAAA | CACTNCCGCA | AAGGTAAAG | GGAACAAACAA | ATTCTNTTTA | 360 |
| CAACANCNC | NATTAAAAA | ATCATATCTC | AAATCTTAGG | GGAAATATATA | CTTCACACNG | 420 |
| GGATCTTAA | TTTACTNCA | CTTTGTTAT | TTTTTANAA | CCATTGTNTT | GGGCCAACAA | 480 |
| CAATGGNAAT | NCCNCCNCC | TGGACTAGT | | | | 509 |

(2) INFORMATION FOR SEQ ID NO:203:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 583 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:203:

| | | | | | | |
|------------|------------|------------|------------|------------|-------------|-----|
| TTTTTTTTT | TTTTTTTG | CCCCCTCTT | ATAAAAACA | AGTTACCATT | TTATTTACT | 60 |
| TACACATATT | TATTITATAA | TTGGTATTAG | ATATTCAAAA | GCGAGCTTTT | AAAATCAAAC | 120 |
| TAATGGAAA | CTGCCTAGA | TACATAATTC | TTAGGAATT | GCTTAAAATC | TGCCCTAAAGT | 180 |
| GAAAATCTC | TCTAGCTCTT | TTGACTGTAA | ATTTTGACT | CTTGTAAAAC | ATCCAAATTC | 240 |
| ATTTTCTTG | TCTTAAAT | TATCTAATCT | TTCCATTTTT | TCCCTATTCC | AAGTCAATT | 300 |
| GCTTCTCTAG | CCTCATTCC | TAGCTCTTAT | CTACTATTAG | TAAGTGGCTT | TTTCCTAAA | 360 |
| AGGGAAAACA | GGAAGAGANA | ATGGCACACA | AAACAAACAT | TTTATATTCA | TAFTTCTACC | 420 |
| TACGTTAATA | AAATAGCATT | TTGTGAAGCC | AGCTAAAAG | AAGGCTTAGA | TCCCTTTATG | 480 |
| TCCATTTAG | TCACTAAACG | ATATCNAAG | TGCCAGAATG | CAAAGGTTT | GTGAACATT | 540 |
| ATCAAAAGC | TAATATAAGA | TATTCACAT | ACTCATCTT | CTG | | 583 |

(2) INFORMATION FOR SEQ ID NO:204:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 589 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:204:

| | | | | | | |
|------------|------------|------------|------------|------------|------------|-----|
| TTTTTTTTNT | TTTTTTTTTT | TTTTTNCTC | TTCTTTTTTT | TTGANAATGA | GGATCGAGTT | 60 |
| TTTCACTCTC | AGATAGGGC | ATGAAGAAAA | CTCATCTTC | CAGCTTAAA | ATAACAATCA | 120 |
| AATCTCTTAT | GCTATATCAT | ATTTAAGTT | AAACTAATGA | GTCACTGGCT | TATCTTCTCC | 180 |
| TGAAGGAAAT | CTGTTCATTC | TTCTCATTCA | TATAGTTATA | TCAAGTACTA | CCTTGCATAT | 240 |
| TGAGAGCTTT | TTCTTCTCTA | TTTACACATA | TATTTCCATG | TGAATTGTA | TCAAACCTTT | 300 |
| ATTTTCATGC | AAACTAGAAA | ATAATGTNTT | CTTTGCATA | AGAGAAGAGA | ACAATATNAG | 360 |
| CATTACAAAA | CTGCTAAAT | TGTTTGTAA | GNTTATCCAT | TATAATTAGT | TNGGCAGGAG | 420 |
| CTAATACAAA | TCACATTAC | NGACNAGCAA | TAATAAAACT | GAAGTACAG | TTAAATATCC | 480 |
| AAAATAATT | AAGAACATT | TTAGGCCCTG | GTATAATTAG | CTAATTCACT | TTACAAGCAT | 540 |
| TTATTNAGAA | TGAATTACA | TGTTATTATT | CCNTAGCCCA | ACACAATGG | | 589 |

(2) INFORMATION FOR SEQ ID NO:205:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 545 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:205:

| | | | | | | |
|------------|------------|------------|------------|------------|------------|-----|
| TTTTTTTTT | TTTTTCAGT | AATAATCAGA | ACAATATT | TTTTTATATT | TAATTCAT | 60 |
| AGAAAAGTGC | CTTACATT | ATAAAAGTT | GTTCCTAA | GTGATCAGAG | GAATTAGATA | 120 |
| TNGTCTTGAA | CACCAATATT | AATTGAGGA | AAATACACCA | AAATACATTA | AGTAAATTAT | 180 |
| TTAAGATCAT | AGAGCTTGTA | AGTAAAAGA | TAATTTGA | CCTCAGAAAC | TCTGAGCATT | 240 |
| AAAATCCAC | TATTAGCAA | TAATTA | TGGACTCTT | GCTTAAATT | TGTGATGAAT | 300 |
| ATGGGGTGTC | ACTGGTAAAC | CAACACATTC | TGAAGGATAC | ATTACTTAGT | GATAGATTCT | 360 |
| TATGTACTTT | GCTANATNAC | GTGGATATGA | GTGACAAGT | TTCTCTTTCT | TCAATCTTT | 420 |
| AAGGGCGNGA | NGAAATGAGG | AAGAAAAGAA | AAGGATTACG | CATACTGTTC | TTTCATNGG | 480 |
| AAGGATTAGA | TATGTTTCCT | TTGCCAATAT | TAAGAAATA | ATAATGTTA | CTACTAGTGA | 540 |
| AACCC | | | | | | 545 |

(2) INFORMATION FOR SEQ ID NO:206:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 487 base pairs

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:206:

| | | | | | | |
|------------|-------------|------------|------------|------------|------------|-----|
| TTTTTTTTT | TTTTTAGTC | AAGTTCTNA | TTTTTATTAT | AATTAAAGTC | TTGGTCATT | 60 |
| CATTTATTAG | CTCTGCAACT | TACATATTAA | AATTAAAGAA | ACGTTNTTAG | ACAACGTNA | 120 |
| CAATTATAA | ATGTAAGGTG | CCATTATTGA | GTANATATAT | TCCTCCAAGA | GTGGATGTGT | 180 |
| CCCTTCTCCC | ACCAACTAAT | GAANCAGCAA | CATTAGTTA | ATTTTATTAG | TAGATNATAC | 240 |
| ACTGCTGCAA | ACGCCAAATTC | TCTTCTCCAT | CCCCATGTNG | ATATTGTGTA | TATGTGTGAG | 300 |
| TTGGTNAGAA | TGCATCANCA | ATCTNACAA | CAACAGCAAG | ATGAAGCTAG | GCNTGGGCTT | 360 |
| TCGGTGAAA | TAGACTGTGT | CTGTCTGAAT | CAAATGATCT | GACCTATCCT | CGGTGGCAAG | 420 |
| AACTCTCGA | ACCGCTTCCT | CAAAGGCNGC | TGCCACATTT | GTGGCNCCTN | TTGCACTTGT | 480 |
| TTCAAAA | | | | | | 487 |

(2) INFORMATION FOR SEQ ID NO:207:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 332 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:207:

| | | | | | | |
|------------|-------------|------------|------------|------------|-------------|-----|
| TGAATTGGCT | AAAAGACTGC | ATTTTANAA | CTAGCAACTC | TTATTTCTTT | CCTTTAAAAAA | 60 |
| TACATAGCAT | AAAATCCAA | ATCCTATTAA | AAGACCTGAC | AGCTTGAGAA | GGTCACTACT | 120 |
| GCATTTATAG | GACCTTCTGG | TGGTTCTGCT | GTACNTTTG | AANTCTGACA | ATCCTTGANA | 180 |
| ATCTTTGCAT | GCAGAGGGAGG | AAAAAGGTAT | TGGATTTCA | CAGAGGAANA | ACACAGCGCA | 240 |
| GAAATGAAGG | GGCCAGGCTT | ACTGAGCTTG | TCCACTGGAG | GGCTCATGGG | TGGGACATGG | 300 |
| AAAAGAAGGC | AGCCTAGGCC | CTGGGGAGCC | CA | | | 332 |

(2) INFORMATION FOR SEQ ID NO:208:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 524 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:208:

| | | | | | | |
|-------------|-------------|------------|------------|-------------|------------|-----|
| AGGGCGTGGT | GCGGAGGGCG | TTACTGTTTT | GTCTCAGTAA | CAATAAAATAC | AAAAAGACTG | 60 |
| GTTGTGTTCC | GGCCCCATCC | AACCACGAAG | TGATTCTC | TTGTGTGCAG | AGTGAAGTGT | 120 |
| TTTAAAGGAC | ATGGAGCTTG | TCACAATGTC | ACAATGTCAC | AGTGTGAAGG | GCACACTCAC | 180 |
| TCCCGCGTGA | TTCACATTTA | GCAACCAACA | ATAGCTCATG | AGTCCATACT | TGTAAATACT | 240 |
| TTTGGCAGAA | TACTTNTTGA | AACTTGCAGA | TGATAACTAA | GATCCAAGAT | ATTTCCCAA | 300 |
| GTAAATAGAA | GTGGGTCTATA | ATATTAATTA | CCTGTTACA | TCAGCTTCCA | TTTACAAGTC | 360 |
| ATGAGCCCCAG | ACACTGACAT | CAAACCAAGC | CCACTTAGAC | TCCTCACAC | CAGTCTGTCC | 420 |
| TGTCATCAGA | CAGGAGGCTG | TCACCTTGAC | CAAATTCTCA | CCAGTCAATC | ATCTATCCAA | 480 |
| AAACCATTAC | CTGATCCACT | TCCGGTAATG | CACCACTTG | GTGA | | 524 |

(2) INFORMATION FOR SEQ ID NO:209:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 159 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:209:

| | |
|---|-----|
| GGGTGAGGAA ATCCAGAGTT GCCATGGAGA AAATTCCAGT GTCAGCATTC TTGCTCCTTG | 60 |
| TGGCCCTCTC CTACACTCTG GCCAGAGATA CCACAGTCAA ACCTGGAGCC AAAAAGGACA | 120 |
| CAAAGGACTC TCGACCCAAA CTGCCCCAGA CCCTCTCCA | 159 |

(2) INFORMATION FOR SEQ ID NO:210:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 256 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:210:

| | |
|---|-----|
| ACTCCCTGGC AGACAAAGGC AGAGGAGAGA GCTCTGTTAG TTCTGTGTTG TTGAAGTGCC | 60 |
| ACTGAATTTC TTTCCACTTG GACTATTACA TGCCANTTGA GGGACTAATG GAAAAACGTA | 120 |
| TGGGGAGATT TTANCAAATT TANGNTNTGA AATGGGGAGA CTGGGGCAGG CGGGAGAGAT | 180 |
| TTGCAGGGTG NAAATGGGAN GGCTGGTTG TTANATGAAC AGGGACATAG GAGGTAGGCA | 240 |
| CCAGGATGCT AAATCA | 256 |

(2) INFORMATION FOR SEQ ID NO:211:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 264 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:211:

| | |
|--|-----|
| ACATTGTTTT TTTGAGATAA AGCATTGAGA GAGCTCTCCT TAACGTGACA CAATGGAAGG | 60 |
| ACTGGAACAC ATACCCACAT CTTTGTCTG AGGGATAATT TTCTGATAAA GTCTTGCTGT | 120 |
| ATATTCAAGC ACATATGTTA TATATTATTC AGTCCATGT TTATAGCCTA GTTAAGGAGA | 180 |
| GGGGAGATAC ATTNCNGAAAG AGGACTGAAA GAAATACTCA AGTNGGAAAA CAGAAAAAGA | 240 |
| AAAAAAGGAG CAAATGAGAA GCCT | 264 |

(2) INFORMATION FOR SEQ ID NO:212:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 328 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:212:

| | |
|---|-----|
| ACCCAAAAAT CCAATGCTGA ATATTTGGCT TCATTATTCC CANATTCTTT GATTGTCAAA | 60 |
| GGATTAATG TTGTCAGC TTGGGCACCTT CAGTTAGGAC CTAAGGATGC CAGCCGGCAG | 120 |
| GTTTATATAT GCAGCAACAA TATTCAAGCG CGACAACAGG TTATTGAACT TGCCCGCCAG | 180 |
| TTNAATTTC A TTCCCATTGA CTTGGGATCC TTATCATCG CCAGAGAGAT TGAAAATTAA | 240 |
| CCCCTACNAC TCTTACTCT CTGGANAGGG CCAGTGGTGG TAGCTATAAG CTTGGCCACA | 300 |
| TTTTTTTTTC CTTTATTCC TTGTCAGA | 328 |

(2) INFORMATION FOR SEQ ID NO:213:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 250 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:213:

| | |
|---|-----|
| ACTTATGAGC AGAGCGACAT ATCCNAGTGT AGACTGAATA AAACTGAATT CTCTCCAGTT | 60 |
| TAAAGCATTG CTCACTGAAG GGATAGAAGT GACTGCCAGG AGGGAAAGTA AGCCAAGGCT | 120 |
| CATTATGCCA AAGGANATAT ACATTTCAAT TCTCCAAACT TCTTCCTCAT TCCAAGAGTT | 180 |
| TTCAATATTT GCATGAACCT GCTGATAANC CATGTTAANA AACAAATATC TCTCTNACCT | 240 |
| TCTCATCGGT | 250 |

(2) INFORMATION FOR SEQ ID NO:214:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 444 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:214:

| | |
|---|-----|
| ACCCAGAACAT CAATGCTGAA TATTTGGCTT CATTATTCCC AGATTCTTG ATTGTCAAAG | 60 |
| GATTAATGT TGTCTCAGCT TGGGCACCTTC AGTTAGGACC TAAGGATGCC AGCCGGCAGG | 120 |
| TTTATATATG CAGCAACAAAT ATTCAAGCGC GACAACAGGT TATTGAACCTT GCCCGCCAGT | 180 |
| TGAATTTCAT TCCCATTGAC TTGGGATCCT TATCATCAGC CANAGAGATT GAAAATTAC | 240 |
| CCCTACGACT CTTTACTCTC TGGAGAGGGC CAGTGGTGGT AGCTATAAGC TTGGCCACAT | 300 |
| TTTTTTTCTC TTATTCCTT TGTCAGAGAT GCGATTTCATC CATATGCTAN AAACCAACAG | 360 |
| AGTGACTTTT ACAAAATTCC TATAGANATT GTGAATAAAA CCTTACCTAT AGTTGCCATT | 420 |
| ACTTTGCTCT CCCTAATATA CCTC | 444 |

(2) INFORMATION FOR SEQ ID NO:215:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 366 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:215:

| | |
|---|-----|
| ACTTATGAGC AGAGCGACAT ATCCAAGTGT ANACTGAATA AAACTGAATT CTCTCCAGTT | 60 |
| TAAAGCATTG CTCACTGAAG GGATAGAAGT GACTGCCAGG AGGGAAAGTA AGCCAAGGCT | 120 |

| | |
|---|-----|
| CATTATGCCA AAGGANATAT ACATTTCAAT TCTCCAAACT TCTTCCTCAT TCCAAGAGTT | 180 |
| TTCATAATTT GCATGAACCT GCTGATAAGC CATGTTGAGA AACAAATATC TCTCTGACCT | 240 |
| TCTCATCGGT AAGCAGAGGC TGAGGCAAC ATGGACCATA GCGAANAAAA AACTTAGTAA | 300 |
| TCCAAGCTGT TTTCTACACT GTAACCAGGT TTCCAACCAA GGTGGAAATC TCCTATACTT | 360 |
| GGTGC | 366 |

(2) INFORMATION FOR SEQ ID NO:216:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 260 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:216:

| | |
|---|-----|
| CTGTATAAAC AGAACTCCAC TGCANGAGGG AGGGCCGGGC CAGGAGAAC TCCGCTTGTC | 60 |
| CAAGACAGGG GCCTAAGGAG GGTCTCCACA CTGCTNNTAA GGGCTNTTNC ATTTTTTTAT | 120 |
| TAATAAAAAG TNNAAAAGGC CTCTTCTCAA CTTTTTCCC TTNGGCTGGA AAATTTAAAA | 180 |
| ATCAAAAATT CCCTNAAGTT NTCAAGCTAT CATATATACT NTATCCTGAA AAAGCAACAT | 240 |
| AATCTTCCT TCCCTCCTT | 260 |

(2) INFORMATION FOR SEQ ID NO:217:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 262 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:217:

| | |
|---|-----|
| ACCTACGTGG GTAAGTTTAN AAATGTATA ATTTCAAGGAA NAGGAACGCA TATAATTGTA | 60 |
| TCTTGCTTAT AATTTCTAT TTTAATAAGG AAATAGCAA TTGGGGTGGG GGGAAATGTAG | 120 |
| GGCATTCTAC AGTTTGAGCA AAATGCAATT AAATGTGGAA GGACAGCACT GAAAAATTAA | 180 |
| ATGAATAATC TGTATGATTA TATGTCTCTA GAGTAGATTT ATAATTAGCC ACTTACCTA | 240 |
| ATATCCTTCA TGCTTGTAAA GT | 262 |

(2) INFORMATION FOR SEQ ID NO:218:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 205 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:218:

| | |
|---|-----|
| ACCAAGGTGG TGCATTACCG GAANTGGATC AANGACACCA TCGTGGCCAA CCCCTGAGCA | 60 |
| CCCCTATCAA CTCCCTTTG TAGTAAACTT GGAACCTTGG AAATGACCAAG GCCAAGACTC | 120 |
| AGGCCTCCCC AGTTCTACTG ACCTTTGTCC TTANGNTNAA NGTCCAGGGT TGCTAGGAAA | 180 |
| ANAAATCAGC AGACACAGGT GTAAA | 205 |

(2) INFORMATION FOR SEQ ID NO:219:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 114 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:219:

| | |
|--|-----|
| TACTGTTTG TCTCAGTAAC AATAAATACA AAAAGACTGG TTGTGTTCCG GCCCCATCCA | 60 |
| ACCACGAAGT TGATTCTCT TGTGTGCAGA GTGACTGATT TTAAAGGACA TGGA | 114 |

(2) INFORMATION FOR SEQ ID NO:220:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 93 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:220:

| | |
|---|----|
| ACTAGCCAGC ACAAAAGGCA GGGTAGCCTG AATTGCTTTC TGCTCTTAC ATTTCTTTA | 60 |
| AAATAAGCAT TTAGTGCTCA GTCCCTACTG AGT | 93 |

(2) INFORMATION FOR SEQ ID NO:221:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 167 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:221:

| | |
|---|-----|
| ACTANGTGCA GGTGCGCACA AATATTTGTC GATATTCCCT TCATCTTGGG TTCCATGAGG | 60 |
| TCTTTGCC AGCCTGTGGC TCTACTGTAG TAAGTTCTG CTGATGAGGA GCCAGNATGC | 120 |
| CCCCCACTAC CTTCCCTGAC GCTCCCCANA AATCACCCAA CCTCTGT | 167 |

(2) INFORMATION FOR SEQ ID NO:222:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 351 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:222:

| | |
|---|-----|
| AGGGCGTGGT GCGGAGGGCG GTACTGACCT CATTAGTAGG AGGATGCATT CTGGCACCCC | 60 |
| GTTCTTCACC TGCCCCCAA TCCTTAAAAG GCCATACTGC ATAAAGTCAA CAACAGATAAA | 120 |
| ATGTTTGCTG AATTAAGGA TGGATGAAAA AAATTAATAA TGAATTTTG CATAATCCAA | 180 |
| TTTCTCTTT TATATTCTA GAAGAAGTTT CTTTGAGCCT ATTAGATCCC GGAAATCTT | 240 |
| TAGGTGAGCA TGATTAGAGA GCTTGAGGT TGCTTTACA TATATCTGGC ATATTTGAGT | 300 |

CTCGTATCAA AACAAATAGAT TGGTAAAGGT GGTATTATTG TATTGATAAG T

351

(2) INFORMATION FOR SEQ ID NO:223

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 383 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:223:

| | |
|---|-----|
| AAAACAAACA AACAAAAAAA ACAATTCTTC ATTCAAGAAA ATTATCTTAG GGACTGATAT | 60 |
| TGGTAATTAT GGTCAATTAA ATWRTRTTK GTGGCATTTTC CTTACATTGT CTTGACAAGA | 120 |
| TTAAAATGTC TGTGCCAAA TTTTGATATT TATTGGAGA CTTCTTATCA AAAGTAATGC | 180 |
| TGCCAAAGGA AGTCTAAGGA ATTAGTAGTG TTCCCMTCAC TTGTTGGAG TGTGCTATT | 240 |
| TAAAAGATT TGATTCCTG GAATGACAAT TATATTTAA CTTTGGTGGG GGAAANAGTT | 300 |
| ATAGGACAC AGTCTTCACT TCTGATACTT GTAAATTAAT CTTTATTGC ACTTGTGTTG | 360 |
| ACCATTAAGC TATATGTTA AAA | 383 |

(2) INFORMATION FOR SEQ ID NO:224

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 320 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:224

| | |
|--|-----|
| CCCCTGAAGG CTTCTTGTTA GAAAATAGTA CAGTTACAAAC CAATAGGAAC AACAAAAAGA | 60 |
| AAAAGTTGT GACATTGTAG TAGGGAGTGT GTACCCCTTA CTCCCCATCA AAAAAAAAT | 120 |
| GGATACATGG TTAAAGGATA RAAGGGCAAT ATTTTATCAT ATGTTCTAAA AGAGAAGGAA | 180 |
| GAGAAAATAC TACTTTCTCR AAATGGAAGC CCTTAAAGGT GCTTTGATAC TGAAGGACAC | 240 |
| AAATGTGGCC GTCCATCCTC CTTTARAGTT GCATGACTTG GACACGGTAA CTGTTGCAGT | 300 |
| TTTARACTCM GCATTGTGAC | 320 |

CLAIMS

1. A polypeptide comprising an immunogenic portion of a prostate protein or a variant thereof, wherein said protein comprises an amino acid sequence encoded by a DNA molecule having a sequence selected from the group consisting of nucleotide sequences recited in SEQ ID NOS: 2, 3, 8-29, 41-45, 47-52, 54-65, 70, 73-74, 79, 81, 87, 90, 92, 93, 97, 103, 104, 107, 109-111, 115-160, 171, 173-175, 177, 181, 188, 191, 193, 194, 198, 203, 204, 207, 209-211, 220, 222-224, the complements of said nucleotide sequences and variants of said nucleotide sequences.

2. A DNA molecule comprising a nucleotide sequence encoding the polypeptide of claim 1.

3. A DNA molecule having a sequence provided in SEQ ID NOS: 2, 3, 8-29, 41-45, 47-52, 54-65, 70, 73-74, 79, 81, 87, 90, 92, 93, 97, 103, 104, 107, 109-111, 115-160, 171, 173-175, 177, 181, 188, 191, 193, 194, 198, 203, 204, 207, 209-211, 220 and 222-224.

4. An expression vector comprising the DNA molecule of claims 2 or 3.

5. A host cell transformed with the expression vector of claim 4.

6. The host cell of claim 5 wherein the host cell is selected from the group consisting of *E. coli*, yeast and mammalian cell lines.

7. A pharmaceutical composition comprising the polypeptide of claim 1 and a physiologically acceptable carrier.

8. A vaccine comprising the polypeptide of claim 1 and a non-specific immune response enhancer.

9. The vaccine of claim 8 wherein the non-specific immune response enhancer is an adjuvant.

10. A vaccine comprising the DNA molecule of claims 2 or 3 and a non-specific immune response enhancer.

11. The vaccine of claim 10 wherein the non-specific immune response enhancer is an adjuvant.

12. A pharmaceutical composition for the treatment of prostate cancer comprising a polypeptide and a physiologically acceptable carrier, the polypeptide comprising an immunogenic portion of a prostate protein or of a variant thereof, wherein said protein comprises an amino acid sequence encoded by a DNA molecule having a sequence selected from the group consisting of nucleotide sequences recited in SEQ ID Nos: 5-7, 30-40, 46, 53, 66-69, 71, 72, 75-78, 80, 82-86, 88, 89, 91, 94-96, 98-102, 105, 106, 161-170, 179, 180, 182-187, 189, 190, 192, 195-197, 199-202, 205, 206, 208, 212-219 and 221, the complements of said nucleotide sequences and variants of said nucleotide sequences.

13. A vaccine for the treatment of prostate cancer comprising a polypeptide and a non-specific immune response enhancer, said polypeptide comprising an immunogenic portion of a prostate protein or a variant thereof, wherein said protein comprises an amino acid sequence encoded by a DNA molecule having a sequence selected from the group consisting of nucleotide sequences recited in SEQ ID Nos: 5-7, 30-40, 46, 53, 66-69, 71, 72, 75-78, 80, 82-86, 88, 89, 91, 94-96, 98-102, 105, 106, 161-170, 179, 180, 182-187, 189, 190, 192, 195-197, 199-202, 205, 206, 208, 212-219, 221, the complements of said nucleotide sequences and variants of said nucleotide sequences

14. The vaccine of claim 13 wherein the non-specific immune response enhancer is an adjuvant.

15. A vaccine for the treatment of prostate cancer comprising a DNA molecule and a non-specific immune response enhancer, the DNA molecule having a sequence selected from the group consisting of nucleotide sequences recited in SEQ ID Nos: 5-7, 30-40, 46, 53, 66-69, 71, 72, 75-78, 80, 82-86, 88, 89, 91, 94-96, 98-102, 105, 106, 161-170, 179, 180, 182-187, 189, 190, 192, 195-197, 199-202, 205, 206, 208, 212-219, 221, the complements of said nucleotide sequences and variants of said nucleotide sequences.

16. The vaccine of claim 15 wherein the non-specific immune response enhancer is an adjuvant.

17. A method for inhibiting the development of prostate cancer in a patient, comprising administering to the patient an effective amount of the pharmaceutical composition of claims 7 or 12.

18. A method for inhibiting the development of prostate cancer in a patient, comprising administering to the patient an effective amount of the vaccine of any one of claims 8, 10, 13 or 15.

19. A fusion protein comprising two or more polypeptides according to claim 1.

20. A fusion protein comprising a polypeptide according to claim 1 and a known prostate antigen.

21. A pharmaceutical composition comprising a fusion protein according to any one of claims 19-20 and a physiologically acceptable carrier.

22. A vaccine comprising a fusion protein according to any one of claims 19-20 and a non-specific immune response enhancer.

23. The vaccine of claim 22 wherein the non-specific immune response enhancer is an adjuvant.

24. A method for inhibiting the development of prostate cancer in a patient, comprising administering to the patient an effective amount of the pharmaceutical composition of claim 21.

25. A method for inhibiting the development of prostate cancer in a patient, comprising administering to the patient an effective amount of the vaccine of claim 22.

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INTERNATIONAL APPLICATION PUBLISHED UNDER THE PATENT COOPERATION TREATY (PCT)

| | | | |
|--|--|--|---|
| (51) International Patent Classification ⁶ : C12N 15/12, C07K 14/705, C12N 5/10, 1/21, A61K 38/17, C12N 1/19, A61K 39/00, C12N 15/62 | | A3 | (11) International Publication Number: WO 98/37093 (43) International Publication Date: 27 August 1998 (27.08.98) |
| (21) International Application Number: PCT/US98/03492 (22) International Filing Date: 25 February 1998 (25.02.98) (30) Priority Data: 08/806,099 25 February 1997 (25.02.97) US 08/904,804 1 August 1997 (01.08.97) US 09/020,956 9 February 1998 (09.02.98) US | | (81) Designated States: AL, AM, AT, AU, BA, BB, BG, BR, BY, CA, CH, CN, CU, CZ, DE, DK, EE, ES, FI, GB, GE, GH, GM, GW, HU, ID, IL, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, UA, UG, UZ, VN, YU, ZW, ARIPO patent (GH, GM, KE, LS, MW, SD, SZ, UG, ZW), Eurasian patent (AM, AZ, BY, KG, KZ, MD, RU, TJ, TM), European patent (AT, BE, CH, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE), OAPI patent (BF, BJ, CF, CG, CI, CM, GA, GN, ML, MR, NE, SN, TD, TG). | |
| (71) Applicant: CORIXA CORPORATION [US/US]; Suite 200, 1124 Columbia Street, Seattle, WA 98104 (US). (72) Inventors: XU, Jiangchun; 15805 Southeast 43rd Place, Bellevue, WA 98006 (US). DILLON, Davin, C.; 21607 N.E. 24th Street, Redmond, WA 98053 (US). (74) Agents: MAKI, David, J. et al.; Seed and Berry LLP, 6300 Columbia Center, 701 Fifth Avenue, Seattle, WA 98104-7092 (US). | | Published <i>With international search report. Before the expiration of the time limit for amending the claims and to be republished in the event of the receipt of amendments.</i> (88) Date of publication of the international search report: 17 December 1998 (17.12.98) | |

(54) Title: COMPOUNDS FOR IMMUNOTHERAPY OF PROSTATE CANCER AND METHODS FOR THEIR USE

(57) Abstract

Compounds and methods for treating prostate cancer are provided. The inventive compounds include polypeptides containing at least a portion of a prostate tumor protein. Vaccines and pharmaceutical compositions for immunotherapy of prostate cancer comprising such polypeptides, or DNA molecules encoding such polypeptides, are also provided, together with DNA molecules for preparing the inventive polypeptides.

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| EE | Estonia | | | | | | |

INTERNATIONAL SEARCH REPORT

| |
|------------------------------|
| International Application No |
| PCT/US 98/03492 |

| A. CLASSIFICATION OF SUBJECT MATTER IPC 6 C12N15/12 C07K14/705 C12N5/10 C12N1/21 A61K38/17 C12N1/19 A61K39/00 C12N15/62 | | | | | | | | | | | | | | | | | | | | | | | |
|---|---|-----------------------|--|--|--|------------|--|-----------------------|---|---|--|---|---|--|---|---|--|---|---|--|--|-----|--|
| According to International Patent Classification (IPC) or to both national classification and IPC | | | | | | | | | | | | | | | | | | | | | | | |
| B. FIELDS SEARCHED Minimum documentation searched (classification system followed by classification symbols) IPC 6 C07K C12N A61K | | | | | | | | | | | | | | | | | | | | | | | |
| Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched | | | | | | | | | | | | | | | | | | | | | | | |
| Electronic data base consulted during the international search (name of data base and, where practical, search terms used) | | | | | | | | | | | | | | | | | | | | | | | |
| C. DOCUMENTS CONSIDERED TO BE RELEVANT <table border="1" style="width: 100%; border-collapse: collapse;"> <thead> <tr> <th style="text-align: left; padding: 2px;">Category *</th> <th style="text-align: left; padding: 2px;">Citation of document, with indication, where appropriate, of the relevant passages</th> <th style="text-align: left; padding: 2px;">Relevant to claim No.</th> </tr> </thead> <tbody> <tr> <td style="padding: 2px;">A</td> <td style="padding: 2px;">WO 95 04548 A (JENNER TECHNOLOGIES) 16 February 1995 see the whole document ---</td> <td style="padding: 2px;"></td> </tr> <tr> <td style="padding: 2px;">A</td> <td style="padding: 2px;">WO 93 25224 A (VETROGEN CORP) 23 December 1993 see the whole document ---</td> <td style="padding: 2px;"></td> </tr> <tr> <td style="padding: 2px;">A</td> <td style="padding: 2px;">WO 95 30758 A (MAYO FOUNDATION ;HYBRITECH INC (US); TINDALL DONALD J (US); YOUNG) 16 November 1995 see the whole document ---</td> <td style="padding: 2px;"></td> </tr> <tr> <td style="padding: 2px;">A</td> <td style="padding: 2px;">EP 0 652 014 A (NAT INST IMMUNOLOGY) 10 May 1995 see the whole document ---</td> <td style="padding: 2px;"></td> </tr> <tr> <td style="padding: 2px;"></td> <td style="padding: 2px; text-align: center;">-/-</td> <td style="padding: 2px;"></td> </tr> </tbody> </table> | | | | | | Category * | Citation of document, with indication, where appropriate, of the relevant passages | Relevant to claim No. | A | WO 95 04548 A (JENNER TECHNOLOGIES) 16 February 1995 see the whole document --- | | A | WO 93 25224 A (VETROGEN CORP) 23 December 1993 see the whole document --- | | A | WO 95 30758 A (MAYO FOUNDATION ;HYBRITECH INC (US); TINDALL DONALD J (US); YOUNG) 16 November 1995 see the whole document --- | | A | EP 0 652 014 A (NAT INST IMMUNOLOGY) 10 May 1995 see the whole document --- | | | -/- | |
| Category * | Citation of document, with indication, where appropriate, of the relevant passages | Relevant to claim No. | | | | | | | | | | | | | | | | | | | | | |
| A | WO 95 04548 A (JENNER TECHNOLOGIES) 16 February 1995 see the whole document --- | | | | | | | | | | | | | | | | | | | | | | |
| A | WO 93 25224 A (VETROGEN CORP) 23 December 1993 see the whole document --- | | | | | | | | | | | | | | | | | | | | | | |
| A | WO 95 30758 A (MAYO FOUNDATION ;HYBRITECH INC (US); TINDALL DONALD J (US); YOUNG) 16 November 1995 see the whole document --- | | | | | | | | | | | | | | | | | | | | | | |
| A | EP 0 652 014 A (NAT INST IMMUNOLOGY) 10 May 1995 see the whole document --- | | | | | | | | | | | | | | | | | | | | | | |
| | -/- | | | | | | | | | | | | | | | | | | | | | | |
| <input checked="" type="checkbox"/> Further documents are listed in the continuation of box C. | | | <input checked="" type="checkbox"/> Patent family members are listed in annex. | | | | | | | | | | | | | | | | | | | | |
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| Date of the actual completion of the international search | | | Date of mailing of the international search report | | | | | | | | | | | | | | | | | | | | |
| 30 July 1998 | | | 03.11.1998 | | | | | | | | | | | | | | | | | | | | |
| Name and mailing address of the ISA European Patent Office, P.B. 5818 Patentlaan 2 NL - 2280 HV Rijswijk Tel. (+31-70) 340-2040, Tx. 31 651 open, Fax: (+31-70) 340-3016 | | | Authorized officer Oderwald, H | | | | | | | | | | | | | | | | | | | | |

INTERNATIONAL SEARCH REPORT

| | |
|-----------------|--------------------|
| Inten | nal Application No |
| PCT/US 98/03492 | |

C.(Continuation) DOCUMENTS CONSIDERED TO BE RELEVANT

| Category * | Citation of document, with indication, where appropriate, of the relevant passages | Relevant to claim No. |
|------------|---|-----------------------|
| X | <p>SHORT J M ET AL: "LAMBDA ZAP: A BACTERIOPHAGE LAMBDA EXPRESSION VECTOR WITH IN VIVO EXCISION PROPERTIES" NUCLEIC ACIDS RESEARCH, vol. 16, no. 15, 1988, pages 7583-7600, XP002007597 see the whole document & "AC No. AA453562" EMBL SEQUENCE DATABASE, 10 May 1990, HEIDELBERG, GERMANY, see nucleotides 398-765</p> <p>---</p> | 2,4-6 |
| X,P | <p>HILLIER L ET AL: "Homo sapiens cDNA clone 788180 (AC No. AA453562)" EMBL SEQUENCE DATABASE, 11 June 1997, HEIDELBERG, GERMANY, XP002073072 see the whole document</p> <p>-----</p> | 2,4-6 |

INTERNATIONAL SEARCH REPORTInt. rational application No.
PCT/US 98/03492**Box I Observations where certain claims were found unsearchable (Continuation of item 1 of first sheet)**

This International Search Report has not been established in respect of certain claims under Article 17(2)(a) for the following reasons:

1. Claims Nos.: because they relate to subject matter not required to be searched by this Authority, namely:
Remark: Although claims 17, 18, 24 and 25 are directed to a method of treatment of the human/animal body, the search has been carried out and based on the alleged effects of the compound/composition.
2. Claims Nos.: because they relate to parts of the International Application that do not comply with the prescribed requirements to such an extent that no meaningful International Search can be carried out, specifically:
3. Claims Nos.: because they are dependent claims and are not drafted in accordance with the second and third sentences of Rule 6.4(a).

Box II Observations where unity of invention is lacking (Continuation of item 2 of first sheet)

This International Searching Authority found multiple inventions in this international application, as follows:

see further information sheet

1. As all required additional search fees were timely paid by the applicant, this International Search Report covers all searchable claims.
2. As all searchable claims could be searched without effort justifying an additional fee, this Authority did not invite payment of any additional fee.
3. As only some of the required additional search fees were timely paid by the applicant, this International Search Report covers only those claims for which fees were paid, specifically claims Nos.:
4. No required additional search fees were timely paid by the applicant. Consequently, this International Search Report is restricted to the invention first mentioned in the claims; it is covered by claims Nos.:

see further information sheet, subject 1.

Remark on Protest

- The additional search fees were accompanied by the applicant's protest.
 No protest accompanied the payment of additional search fees.

FURTHER INFORMATION CONTINUED FROM PCT/ISA/ 210

This International Searching Authority found multiple (groups of) inventions in this international application, as follows:

1. Claims: 1-11 and 17-25 all partially

A polypeptide comprising an immunogenic portion or a variant of a prostate protein encoded by SEQ ID NO:2, DNA molecules related to said protein, expression vectors comprising said DNA molecules, hosts transformed with said vectors, fusion proteins comprising said polypeptide, pharmaceutical compositions and vaccines comprising said polypeptide, fusion proteins and DNA.

2. Claims: 1-11 and 17-25 all partially

same as invention 1 but for SEQ ID NO: 3.

3. Claims: 1-11 and 17-25 all partially

same as invention 1 but for SEQ ID NO: 8.

4. Claims: 1-11 and 17-25 all partially

same as invention 1 but for SEQ ID NO: 9.

5. Claims: 1-11 and 17-25 all partially

same as invention 1 but for SEQ ID NO: 10.

6. Claims: 1-11 and 17-25 all partially

same as invention 1 but for SEQ ID NO: 11.

7. Claims: 1-11 and 17-25 all partially

same as invention 1 but for SEQ ID NO: 12.

8. Claims: 1-11 and 17-25 all partially

same as invention 1 but for SEQ ID NO: 13.

9. Claims: 1-11 and 17-25 all partially

same as invention 1 but for SEQ ID NO: 14.

10. Claims: 1-11 and 17-25 all partially

FURTHER INFORMATION CONTINUED FROM PCT/ISA/ 210

same as invention 1 but for SEQ ID NO: 15.

11. Claims: 1-11 and 17-25 all partially
same as invention 1 but for SEQ ID NO: 16.

12. Claims: 1-11 and 17-25 all partially
same as invention 1 but for SEQ ID NO: 17.

13. Claims: 1-11 and 17-25 all partially
same as invention 1 but for SEQ ID NO: 18.

14. Claims: 1-11 and 17-25 all partially
same as invention 1 but for SEQ ID NO: 19.

15. Claims: 1-11 and 17-25 all partially
same as invention 1 but for SEQ ID NO: 20.

16. Claims: 1-11 and 17-25 all partially
same as invention 1 but for SEQ ID NO: 21.

17. Claims: 1-11 and 17-25 all partially
same as invention 1 but for SEQ ID NO: 22.

18. Claims: 1-11 and 17-25 all partially
same as invention 1 but for SEQ ID NO: 23.

19. Claims: 1-11 and 17-25 all partially
same as invention 1 but for SEQ ID NO: 24.

20. Claims: 1-11 and 17-25 all partially
same as invention 1 but for SEQ ID NO: 25.

21. Claims: 1-11 and 17-25 all partially

FURTHER INFORMATION CONTINUED FROM PCT/ISA/ 210

- same as invention 1 but for SEQ ID NO: 26.
22. Claims: 1-11 and 17-25 all partially
same as invention 1 but for SEQ ID NO: 27.
23. Claims: 1-11 and 17-25 all partially
same as invention 1 but for SEQ ID NO: 28.
24. Claims: 1-11 and 17-25 all partially
same as invention 1 but for SEQ ID NO: 29.
25. Claims: 1-11 and 17-25 all partially
same as invention 1 but for SEQ ID NO: 41.
26. Claims: 1-11 and 17-25 all partially
same as invention 1 but for SEQ ID NO: 42.
27. Claims: 1-11 and 17-25 all partially
same as invention 1 but for SEQ ID NO: 43.
28. Claims: 1-11 and 17-25 all partially
same as invention 1 but for SEQ ID NO: 44.
29. Claims: 1-11 and 17-25 all partially
same as invention 1 but for SEQ ID NO: 45.
30. Claims: 1-11 and 17-25 all partially
same as invention 1 but for SEQ ID NO: 47.
31. Claims: 1-11 and 17-25 all partially
same as invention 1 but for SEQ ID NO: 48.
32. Claims: 1-11 and 17-25 all partially

FURTHER INFORMATION CONTINUED FROM PCT/ISA/ 210

same as invention 1 but for SEQ ID NO: 49.

33. Claims: 1-11 and 17-25 all partially
same as invention 1 but for SEQ ID NO: 50.

34. Claims: 1-11 and 17-25 all partially
same as invention 1 but for SEQ ID NO: 51.

35. Claims: 1-11 and 17-25 all partially
same as invention 1 but for SEQ ID NO: 52.

36. Claims: 1-11 and 17-25 all partially
same as invention 1 but for SEQ ID NO: 54.

37. Claims: 1-11 and 17-25 all partially
same as invention 1 but for SEQ ID NO: 55.

38. Claims: 1-11 and 17-25 all partially
same as invention 1 but for SEQ ID NO: 56.

39. Claims: 1-11 and 17-25 all partially
same as invention 1 but for SEQ ID NO: 57.

40. Claims: 1-11 and 17-25 all partially
same as invention 1 but for SEQ ID NO: 58.

41. Claims: 1-11 and 17-25 all partially
same as invention 1 but for SEQ ID NO: 59.

42. Claims: 1-11 and 17-25 all partially
same as invention 1 but for SEQ ID NO: 60.

43. Claims: 1-11 and 17-25 all partially

FURTHER INFORMATION CONTINUED FROM PCT/ISA/ 210

same as invention 1 but for SEQ ID NO: 61.

44. Claims: 1-11 and 17-25 all partially
same as invention 1 but for SEQ ID NO: 62.

45. Claims: 1-11 and 17-25 all partially
same as invention 1 but for SEQ ID NO: 63.

46. Claims: 1-11 and 17-25 all partially
same as invention 1 but for SEQ ID NO: 64.

47. Claims: 1-11 and 17-25 all partially
same as invention 1 but for SEQ ID NO: 65.

48. Claims: 1-11 and 17-25 all partially
same as invention 1 but for SEQ ID NO: 70.

49. Claims: 1-11 and 17-25 all partially
same as invention 1 but for SEQ ID NO: 73.

50. Claims: 1-11 and 17-25 all partially
same as invention 1 but for SEQ ID NO: 74.

51. Claims: 1-11 and 17-25 all partially
same as invention 1 but for SEQ ID NO: 79.

52. Claims: 1-11 and 17-25 all partially
same as invention 1 but for SEQ ID NO: 81.

53. Claims: 1-11 and 17-25 all partially
same as invention 1 but for SEQ ID NO: 87.

54. Claims: 1-11 and 17-25 all partially

FURTHER INFORMATION CONTINUED FROM PCT/ISA/ 210

- same as invention 1 but for SEQ ID NO: 90.
55. Claims: 1-11 and 17-25 all partially
same as invention 1 but for SEQ ID NO: 92.
56. Claims: 1-11 and 17-25 all partially
same as invention 1 but for SEQ ID NO: 93.
57. Claims: 1-11 and 17-25 all partially
same as invention 1 but for SEQ ID NO: 97.
58. Claims: 1-11 and 17-25 all partially
same as invention 1 but for SEQ ID NO: 103.
59. Claims: 1-11 and 17-25 all partially
same as invention 1 but for SEQ ID NO: 104.
60. Claims: 1-11 and 17-25 all partially
same as invention 1 but for SEQ ID NO: 107.
61. Claims: 1-11 and 17-25 all partially
same as invention 1 but for SEQ ID NO: 109.
62. Claims: 1-11 and 17-25 all partially
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63. Claims: 1-11 and 17-25 all partially
same as invention 1 but for SEQ ID NO: 111.
64. Claims: 1-11 and 17-25 all partially
same as invention 1 but for SEQ ID NO: 115.
65. Claims: 1-11 and 17-25 all partially

FURTHER INFORMATION CONTINUED FROM PCT/ISA/ 210

- same as invention 1 but for SEQ ID NO: 116.
66. Claims: 1-11 and 17-25 all partially
same as invention 1 but for SEQ ID NO: 117.
67. Claims: 1-11 and 17-25 all partially
same as invention 1 but for SEQ ID NO: 118.
68. Claims: 1-11 and 17-25 all partially
same as invention 1 but for SEQ ID NO: 119.
69. Claims: 1-11 and 17-25 all partially
same as invention 1 but for SEQ ID NO: 120.
70. Claims: 1-11 and 17-25 all partially
same as invention 1 but for SEQ ID NO: 121.
71. Claims: 1-11 and 17-25 all partially
same as invention 1 but for SEQ ID NO: 122.
72. Claims: 1-11 and 17-25 all partially
same as invention 1 but for SEQ ID NO: 123.
73. Claims: 1-11 and 17-25 all partially
same as invention 1 but for SEQ ID NO: 124.
74. Claims: 1-11 and 17-25 all partially
same as invention 1 but for SEQ ID NO: 125.
75. Claims: 1-11 and 17-25 all partially
same as invention 1 but for SEQ ID NO: 126.
76. Claims: 1-11 and 17-25 all partially

FURTHER INFORMATION CONTINUED FROM PCT/ISA/ 210

same as invention 1 but for SEQ ID NO: 127.

77. Claims: 1-11 and 17-25 all partially
same as invention 1 but for SEQ ID NO: 128.

78. Claims: 1-11 and 17-25 all partially
same as invention 1 but for SEQ ID NO: 129.

79. Claims: 1-11 and 17-25 all partially
same as invention 1 but for SEQ ID NO: 130.

80. Claims: 1-11 and 17-25 all partially
same as invention 1 but for SEQ ID NO: 131.

81. Claims: 1-11 and 17-25 all partially
same as invention 1 but for SEQ ID NO: 132.

82. Claims: 1-11 and 17-25 all partially
same as invention 1 but for SEQ ID NO: 133.

83. Claims: 1-11 and 17-25 all partially
same as invention 1 but for SEQ ID NO: 134.

84. Claims: 1-11 and 17-25 all partially
same as invention 1 but for SEQ ID NO: 135.

85. Claims: 1-11 and 17-25 all partially
same as invention 1 but for SEQ ID NO: 136.

86. Claims: 1-11 and 17-25 all partially
same as invention 1 but for SEQ ID NO: 137.

87. Claims: 1-11 and 17-25 all partially

FURTHER INFORMATION CONTINUED FROM PCT/ISA/ 210

same as invention 1 but for SEQ ID NO: 138.

88. Claims: 1-11 and 17-25 all partially
same as invention 1 but for SEQ ID NO: 139.

89. Claims: 1-11 and 17-25 all partially
same as invention 1 but for SEQ ID NO: 140.

90. Claims: 1-11 and 17-25 all partially
same as invention 1 but for SEQ ID NO: 141.

91. Claims: 1-11 and 17-25 all partially
same as invention 1 but for SEQ ID NO: 142.

92. Claims: 1-11 and 17-25 all partially
same as invention 1 but for SEQ ID NO: 143.

93. Claims: 1-11 and 17-25 all partially
same as invention 1 but for SEQ ID NO: 144.

94. Claims: 1-11 and 17-25 all partially
same as invention 1 but for SEQ ID NO: 145.

95. Claims: 1-11 and 17-25 all partially
same as invention 1 but for SEQ ID NO: 146.

96. Claims: 1-11 and 17-25 all partially
same as invention 1 but for SEQ ID NO: 147.

97. Claims: 1-11 and 17-25 all partially
same as invention 1 but for SEQ ID NO: 148.

98. Claims: 1-11 and 17-25 all partially

FURTHER INFORMATION CONTINUED FROM PCT/ISA/ 210

same as invention 1 but for SEQ ID NO: 149.

99. Claims: 1-11 and 17-25 all partially
same as invention 1 but for SEQ ID NO: 150.

100. Claims: 1-11 and 17-25 all partially
same as invention 1 but for SEQ ID NO: 151.

101. Claims: 1-11 and 17-25 all partially
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102. Claims: 1-11 and 17-25 all partially
same as invention 1 but for SEQ ID NO: 153.

103. Claims: 1-11 and 17-25 all partially
same as invention 1 but for SEQ ID NO: 154.

104. Claims: 1-11 and 17-25 all partially
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105. Claims: 1-11 and 17-25 all partially
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106. Claims: 1-11 and 17-25 all partially
same as invention 1 but for SEQ ID NO: 157.

107. Claims: 1-11 and 17-25 all partially
same as invention 1 but for SEQ ID NO: 158.

108. Claims: 1-11 and 17-25 all partially
same as invention 1 but for SEQ ID NO: 159.

109. Claims: 1-11 and 17-25 all partially

FURTHER INFORMATION CONTINUED FROM PCT/ISA/ 210

same as invention 1 but for SEQ ID NO: 160.

110. Claims: 1-11 and 17-25 all partially
same as invention 1 but for SEQ ID NO: 171.

111. Claims: 1-11 and 17-25 all partially
same as invention 1 but for SEQ ID NO: 173.

112. Claims: 1-11 and 17-25
same as invention 1 but for SEQ ID NO: 174.

113. Claims: 1-11 and 17-25 all partially
same as invention 1 but for SEQ ID NO: 175.

114. Claims: 1-11 and 17-25 all partially
same as invention 1 but for SEQ ID NO: 177.

115. Claims: 1-11 and 17-25
same as invention 1 but for SEQ ID NO: 181.

116. Claims: 1-11 and 17-25 all partially
same as invention 1 but for SEQ ID NO: 188.

117. Claims: 1-11 and 17-25 all partially
same as invention 1 but for SEQ ID NO: 191.

118. Claims: 1-11 and 17-25 all partially
same as invention 1 but for SEQ ID NO: 193.

119. Claims: 1-11 and 17-25 all partially
same as invention 1 but for SEQ ID NO: 194.

120. Claims: 1-11 and 17-25 all partially

FURTHER INFORMATION CONTINUED FROM PCT/ISA/ 210

same as invention 1 but for SEQ ID NO: 198.

121. Claims: 1-11 and 17-25 all partially
same as invention 1 but for SEQ ID NO: 203.

122. Claims: 1-11 and 17-25 all partially
same as invention 1 but for SEQ ID NO: 204.

123. Claims: 1-11 and 17-25 all partially
same as invention 1 but for SEQ ID NO: 207.

124. Claims: 1-11 and 17-25 all partially
same as invention 1 but for SEQ ID NO: 209.

125. Claims: 1-11 and 17-25 all partially
same as invention 1 but for SEQ ID NO: 210.

126. Claims: 1-11 and 17-25 all partially
same as invention 1 but for SEQ ID NO: 211.

127. Claims: 1-11 and 17-25 all partially
same as invention 1 but for SEQ ID NO: 220.

128. Claims: 1-11 and 17-25 all partially
same as invention 1 but for SEQ ID NO: 222.

129. Claims: 1-11 and 17-25 all partially
same as invention 1 but for SEQ ID NO: 223.

130. Claims: 1-11 and 17-25 all partially
same as invention 1 but for SEQ ID NO: 224.

131. Claims: 12-18 all partially

FURTHER INFORMATION CONTINUED FROM PCT/ISA/ 210

Pharmaceutical compositions and a vaccines comprising an immunogenic portion or a variant of a prostate-specific polypeptide and related DNA sequences, said DNA sequences recited in SEQ ID NO: 5.

132. Claims: 12-18 all partially
same as invention 131 but for SEQ ID NO: 6.

133. Claims: 12-18 all partially
same as invention 131 but for SEQ ID NO: 7.

134. Claims: 12-18 all partially
same as invention 131 but for SEQ ID NO: 30.

135. Claims: 12-18 all partially
same as invention 131 but for SEQ ID NO: 31.

136. Claims: 12-18 all partially
same as invention 131 but for SEQ ID NO: 32.

137. Claims: 12-18 all partially
same as invention 131 but for SEQ ID NO: 33.

138. Claims: 12-18 all partially
same as invention 131 but for SEQ ID NO: 34.

139. Claims: 12-18 all partially
same as invention 131 but for SEQ ID NO: 35.

140. Claims: 12-18 all partially
same as invention 131 but for SEQ ID NO: 36.

141. Claims: 12-18 all partially
same as invention 131 but for SEQ ID NO: 37.

FURTHER INFORMATION CONTINUED FROM PCT/ISA/ 210

142. Claims: 12-18 all partially
same as invention 131 but for SEQ ID NO: 38.

143. Claims: 12-18 all partially
same as invention 131 but for SEQ ID NO: 39.

144. Claims: 12-18 all partially
same as invention 131 but for SEQ ID NO: 40.

145. Claims: 12-18 all partially
same as invention 131 but for SEQ ID NO: 46.

146. Claims: 12-18 all partially
same as invention 131 but for SEQ ID NO: 53.

147. Claims: 12-18 all partially
same as invention 131 but for SEQ ID NO: 66.

148. Claims: 12-18 all partially
same as invention 131 but for SEQ ID NO: 67.

149. Claims: 12-18 all partially
same as invention 131 but for SEQ ID NO: 68.

150. Claims: 12-18 all partially
same as invention 131 but for SEQ ID NO: 69.

151. Claims: 12-18 all partially
same as invention 131 but for SEQ ID NO: 71.

152. Claims: 12-18 all partially
same as invention 131 but for SEQ ID NO: 72.

FURTHER INFORMATION CONTINUED FROM PCT/ISA/ 210

153. Claims: 12-18 all partially
same as invention 131 but for SEQ ID NO: 75.
154. Claims: 12-18 all partially
same as invention 131 but for SEQ ID NO: 76.
155. Claims: 12-18 all partially
same as invention 131 but for SEQ ID NO: 77.
156. Claims: 12-18 all partially
same as invention 131 but for SEQ ID NO: 78.
157. Claims: 12-18 all partially
same as invention 131 but for SEQ ID NO: 80.
158. Claims: 12-18 all partially
same as invention 131 but for SEQ ID NO: 82.
159. Claims: 12-18 all partially
same as invention 131 but for SEQ ID NO: 83.
160. Claims: 12-18 all partially
same as invention 131 but for SEQ ID NO: 84.
161. Claims: 12-18 all partially
same as invention 131 but for SEQ ID NO: 85.
162. Claims: 12-18 all partially
same as invention 131 but for SEQ ID NO: 86.
163. Claims: 12-18 all partially
same as invention 131 but for SEQ ID NO: 88.

FURTHER INFORMATION CONTINUED FROM PCT/ISA/ 210

164. Claims: 12-18 all partially
same as invention 131 but for SEQ ID NO: 89.

165. Claims: 12-18 all partially
same as invention 131 but for SEQ ID NO: 91.

166. Claims: 12-18 all partially
same as invention 131 but for SEQ ID NO: 94.

167. Claims: 12-18 all partially
same as invention 131 but for SEQ ID NO: 95.

168. Claims: 12-18 all partially
same as invention 131 but for SEQ ID NO: 96.

169. Claims: 12-18 all partially
same as invention 131 but for SEQ ID NO: 98.

170. Claims: 12-18 all partially
same as invention 131 but for SEQ ID NO: 99.

171. Claims: 12-18 all partially
same as invention 131 but for SEQ ID NO: 100.

172. Claims: 12-18 all partially
same as invention 131 but for SEQ ID NO: 101.

173. Claims: 12-18 all partially
same as invention 131 but for SEQ ID NO: 102.

174. Claims: 12-18 all partially
same as invention 131 but for SEQ ID NO: 105.

FURTHER INFORMATION CONTINUED FROM PCT/ISA/ 210

175. Claims: 12-18 all partially
same as invention 131 but for SEQ ID NO: 106.

176. Claims: 12-18 all partially
same as invention 131 but for SEQ ID NO: 161.

177. Claims: 12-18 all partially
same as invention 131 but for SEQ ID NO: 162.

178. Claims: 12-18 all partially
same as invention 131 but for SEQ ID NO: 163.

179. Claims: 12-18 all partially
same as invention 131 but for SEQ ID NO: 164.

180. Claims: 12-18 all partially
same as invention 131 but for SEQ ID NO: 165.

181. Claims: 12-18 all partially
same as invention 131 but for SEQ ID NO: 166.

182. Claims: 12-18 all partially
same as invention 131 but for SEQ ID NO: 167.

183. Claims: 12-18 all partially
same as invention 131 but for SEQ ID NO: 168.

184. Claims: 12-18 all partially
same as invention 131 but for SEQ ID NO: 169.

185. Claims: 12-18 all partially
same as invention 131 but for SEQ ID NO: 170.

FURTHER INFORMATION CONTINUED FROM PCT/ISA/ 210

186. Claims: 12-18 all partially
same as invention 131 but for SEQ ID NO: 179.

187. Claims: 12-18 all partially
same as invention 131 but for SEQ ID NO: 180.

188. Claims: 12-18 all partially
same as invention 131 but for SEQ ID NO: 182.

189. Claims: 12-18 all partially
same as invention 131 but for SEQ ID NO: 183.

190. Claims: 12-18 all partially
same as invention 131 but for SEQ ID NO: 184.

191. Claims: 12-18 all partially
same as invention 131 but for SEQ ID NO: 185.

192. Claims: 12-18 all partially
same as invention 131 but for SEQ ID NO: 186.

193. Claims: 12-18 all partially
same as invention 131 but for SEQ ID NO: 187.

194. Claims: 12-18 all partially
same as invention 131 but for SEQ ID NO: 189.

195. Claims: 12-18 all partially
same as invention 131 but for SEQ ID NO: 190.

196. Claims: 12-18 all partially
same as invention 131 but for SEQ ID NO: 192.

FURTHER INFORMATION CONTINUED FROM PCT/ISA/ 210

197. Claims: 12-18 all partially
same as invention 131 but for SEQ ID NO: 195.

198. Claims: 12-18 all partially
same as invention 131 but for SEQ ID NO: 196.

199. Claims: 12-18 all partially
same as invention 131 but for SEQ ID NO: 197.

200. Claims: 12-18 all partially
same as invention 131 but for SEQ ID NO: 199.

201. Claims: 12-18 all partially
same as invention 131 but for SEQ ID NO: 200.

202. Claims: 12-18 all partially
same as invention 131 but for SEQ ID NO: 201.

203. Claims: 12-18 all partially
same as invention 131 but for SEQ ID NO: 202.

204. Claims: 12-18 all partially
same as invention 131 but for SEQ ID NO: 205.

205. Claims: 12-18 all partially
same as invention 131 but for SEQ ID NO: 206.

206. Claims: 12-18 all partially
same as invention 131 but for SEQ ID NO: 208.

207. Claims: 12-18 all partially
same as invention 131 but for SEQ ID NO: 212.

FURTHER INFORMATION CONTINUED FROM PCT/ISA/ 210

208. Claims: 12-18 all partially
same as invention 131 but for SEQ ID NO: 213.
209. Claims: 12-18 all partially
same as invention 131 but for SEQ ID NO: 214.
210. Claims: 12-18 all partially
same as invention 131 but for SEQ ID NO: 215.
211. Claims: 12-18 all partially
same as invention 131 but for SEQ ID NO: 216.
212. Claims: 12-18 all partially
same as invention 131 but for SEQ ID NO: 217.
213. Claims: 12-18 all partially
same as invention 131 but for SEQ ID NO: 218.
214. Claims: 12-18 all partially
same as invention 131 but for SEQ ID NO: 219.
215. Claims: 12-18 all partially
same as invention 131 but for SEQ ID NO: 221.

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